

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:18:56 ; Search time 50 Seconds
(without alignments)
950.583 Million cell updates/sec

Title: US-09-462-416A-7
Perfect score: 2861
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSFKFLOSSLRALRQM 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pdp:*
2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pdp:*
3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pdp:*
4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pdp:*
5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCRUS COMB.pdp:*
6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pdp:*
7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1921	67.1	592	2	US-09-313-942-8
2	1921	67.1	592	2	US-10-282-162-8
3	1918	67.0	468	2	US-08-795-473B-5
4	1918	67.0	468	2	US-09-439-856-5
5	1918	67.0	468	2	US-09-949-016-5959
6	1918	67.0	468	7	5480796
7	1918	67.0	468	7	5480796-2
8	1910	66.8	360	2	US-09-313-942-15
9	1910	66.8	360	2	US-10-282-162-15
10	1852	64.7	344	7	5171840-7
11	1852	64.7	344	7	5480796-7
12	1788	62.5	1158	2	US-09-313-942-26
13	1788	62.5	1158	2	US-10-282-162-26
14	1783	62.3	1168	2	US-09-313-942-24
15	1783	62.3	1168	2	US-10-282-162-24
16	1741	60.9	323	7	5171840-6
17	1741	60.9	323	7	5480796-6
18	1683	58.8	315	2	US-09-313-942-16
19	1683	58.8	315	2	US-10-282-162-16
20	1481.5	51.8	388	2	US-09-949-016-9852
21	1389	48.5	386	7	5171840-5
22	1389	48.5	386	7	5480796-5
23	1153	40.3	210	7	US-09-043-785-1
24	950	33.2	201	7	5171840-11
25	939	32.8	185	1	US-08-716-317-7
26	938.5	32.8	212	1	US-08-792-019B-9

27	938.5	32.8	212	2	US-08-988-819-9	Sequence 9, Appli
28	938.5	32.8	212	2	US-09-016-534-9	Sequence 9, Appli
29	938.5	32.8	212	2	US-08-097-869-7	Sequence 7, Appli
30	938.5	32.8	212	2	US-08-795-473B-6	Sequence 6, Appli
31	938.5	32.8	212	2	US-09-230-637-45	Sequence 45, Appli
32	938.5	32.8	212	2	US-09-230-371A-27	Sequence 27, Appli
33	938.5	32.8	212	2	US-09-439-856-6	Sequence 6, Appli
34	938.5	32.8	212	2	US-09-462-941-13	Sequence 13, Appli
35	938.5	32.8	212	7	5510472-2	Patent No. 5510472
36	938.5	32.8	232	2	US-09-949-016-10315	Sequence 10315, A
37	935	32.7	317	2	US-08-469-318-145	Sequence 145, App
38	935	32.7	317	2	US-08-468-609A-145	Sequence 145, App
39	935	32.7	317	2	US-08-446-872A-145	Sequence 145, App
40	935	32.7	317	2	US-08-762-227A-145	Sequence 145, App
41	935	32.7	317	5	PCT-US95-01185-145	Sequence 145, App
42	934	32.6	184	1	US-08-567-047-2	Sequence 2, Appli
43	934	32.6	184	1	US-08-567-048-2	Sequence 2, Appli
44	934	32.6	184	7	5186931-1	Patent No. 5186931
45	934	32.6	185	1	US-07-632-070B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-313-942-8
; Sequence 8, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-8

Query Match		67.1%	Score 1921;	DB 2;	Length 592;
Best Local Similarity		77.1%;	Pred. NO. 8.3e-151;		
Matches 377;		Conservative 22;	Mismatches 44;	Indels 46;	Gaps 5;
QY	1	MLAVGCALLAALLAAPGAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60		
DB	1	MVAVGCALLAALLAAPGAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM	60		
QY	61	VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS	120		
DB	61	VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEQLS	120		
QY	121	CFKPSPLSNVVCWGMGRSTPSLTTKAVLLVRKFKQNSPAEDFOEPCQYQSQKFSQCLAV	180		
DB	121	CFKPSPLSNVVCWGMGRSTPSLTTKAVLLVRKFKQNSPAEDFOEPCQYQSQKFSQCLAV	180		
QY	181	PEGSSFFIVSMCVASSVGSFKSTQTFQGGILOPDPANITVTAVARNPRLSVTWOD	240		
DB	181	PEGSSFFIVSMCVASSVGSFKSTQTFQGGILOPDPANITVTAVARNPRLSVTWOD	240		
QY	241	PHSNSSFYRLRFEURYRAESKTFITWMVKDLQHCVTHDAWSGLRHVVQLRAQEEFQ	300		
DB	241	PHSNSSFYRLRFEURYRAESKTFITWMVKDLQHCVTHDAWSGLRHVVQLRAQEEFQ	300		
QY	301	GEWSSESPAMGTPWTESRPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPYEFMP	360		
DB	301	GEWSSESPAMGTPWTESRPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPYEFMP	360		

Db 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 357
Qy 361 VPPGSDKDVAAHPHQPLTSSRIDKQIRYILDGISALRKETCNKSNMCE--SSKEALAE 418
Db 358 -----DAGEP-----KSCDKTHTCCPPCAPPELLGG 382
Qy 419 NNLLPKMAEKDGCQFQGNBETCLVKIIT---GLLEFEVYLEYLO---NRFESSEBOAR 472
Db 383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 442
Qy 473 AVQMSTKVL 481
Db 443 STYRVWSVL 451

RESULT 2
US-10-282-162-8
; Sequence 8, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-8

Query Match 67.1%; Score 1921; DB 2; Length 592;
Best Local Similarity 77.1%; Pred. No. 8.3e-151;
Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

Qy 1 MLAVGCALLAALAAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALAAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFCQLAV 180
Qy 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITTVARNPRWLVSVTWQD 240
Db 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITTVARNPRWLVSVTWQD 240
Qy 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLOHHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Db 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLOHHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Qy 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 357
Db 361 VPPGSDKDVAAHPHQPLTSSRIDKQIRYILDGISALRKETCNKSNMCE--SSKEALAE 418
Db 358 -----DAGEP-----KSCDKTHTCCPPCAPPELLGG 382
Qy 419 NNLLPKMAEKDGCQFQGNBETCLVKIIT---GLLEFEVYLEYLO---NRFESSEBOAR 472
Db 383 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 442

Qy 473 AVQMSTKVL 481
Db 443 STYRVWSVL 451

RESULT 3
US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Eithan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
US-08-795-473B-5

Query Match 67.0%; Score 1918; DB 2; Length 468;
Best Local Similarity 96.5%; Pred. No. 1e-150;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 MLAVGCALLAALAAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALAAAPGAALAPRCPAQAEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFCQLAV 180
Qy 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITTVARNPRWLVSVTWQD 240
Db 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPPDPANITTVARNPRWLVSVTWQD 240
Qy 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLOHHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Db 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLOHHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Qy 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQ--- 360

Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356

Qy 361 VPPGEDSKDVAAP 373

Db 357 ----QDSSSVPLP 365

RESULT 4

US-09-439-856-5

; Sequence 5, Application US/09439856

; Patent No. 6410009

; GENERAL INFORMATION:

; APPLICANT: Galun, Ethan

; APPLICANT: Nahot, Orit

; APPLICANT: Blum, Herbert E.

; TITLE OF INVENTION: A Pharmaceutical Composition for Treating

; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESS: Davidson, Davidson and Kappel, LLC

; STREET: 1140 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS-DOS EDITOR

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/439,856

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,473

; FILING DATE: 11-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Davidson, Clifford M.

; REGISTRATION NUMBER: 32,728

; REFERENCE/DOCKET NUMBER: 963.1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)-997-1028

; TELEFAX: (212)-997-1037

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 468 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

US-09-439-856-5

Query Match 67.0%; Score 1918; DB 2; Length 468;

Best Local Similarity 96.5%; Pred. No. 1e-150;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180

Qy 181 PEGDSSFIVSMCVASSVGSKFSKTQTQGGCGILOPDPANITVTAVARNPWLVSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVGSKFSKTQTQGGCGILOPDPANITVTAVARNPWLVSVTWOD 240

Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Qy 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVVEFMP 360

Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356

Qy 361 VPPGEDSKDVAAP 373

Db 357 ----QDSSSVPLP 365

RESULT 5

US-09-949-016-5959

; Sequence 5959, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5959

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-5959

Query Match 67.0%; Score 1918; DB 2; Length 468;

Best Local Similarity 96.5%; Pred. No. 1e-150;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAPGAALAPRRCPAOEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYQSOESQKFSQCLAV 180

Qy 181 PEGDSSFIVSMCVASSVGSKFSKTQTQGGCGILOPDPANITVTAVARNPWLVSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVGSKFSKTQTQGGCGILOPDPANITVTAVARNPWLVSVTWOD 240

Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLOHHCVIHDAWSGLRHVVQVLAQEEFQ 300

Qy 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVVEFMP 360

Db 301 GEWSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILFRDSANATSLPV----- 356

Qy 361 VPPGEDSKDVAAP 373

Db 357 ----QDSSSVPLP 365

RESULT 6

5171840-2

; Patent No. 5171840

; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

; STIMULATORY FACTOR-2

; NUMBER OF SEQUENCES: 11

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/298,694

; FILING DATE: 19-JAN-1989

; SEQ ID NO:2:

; LENGTH: 468

5171840-2

Query Match 67.0%; Score 1918; DB 7; Length 468;

Best Local Similarity 96.5%; Pred. No. 1e-150;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

DB 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

QY 361 VPPGEDSKOVAAP 373

DB 357 ---QDSSSVPLP 365

RESULT 7

5480796-2

; Patent No. 5480796

; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

; FOR HUMAN B CELL STIMULATORY FACTOR-2

; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/907,650

; FILING DATE: 02-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 298,694

; FILING DATE: 19-JAN-1989

; SEQ ID NO:2:

; LENGTH: 468

5480796-2

Query Match

Best Local Similarity 67.0%; Score 1918; DB 7; Length 468;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

DB 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360

QY 361 VPPGEDSKOVAAP 373

DB 357 ---QDSSSVPLP 365

RESULT 8

US-09-313-942-15

; Sequence 15, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; FILE REFERENCE: REG 203-A

; CURRENT APPLICATION NUMBER: US/09/313,942

; CURRENT FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 09/313,942

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: 60/101,858

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Fast-Seq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-313-942-15

Query Match 66.8%; Score 1910; DB 2; Length 360;

Best Local Similarity 99.4%; Pred. No. 3.2e-150;

Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

DB 1 MVAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

DB 61 VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPOLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKESCQLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILQDPPANITVAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

DB 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHHCVIHDAMSGLRHVVLQRAQEFPG 300

QY 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

DB 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 9

US-10-282-162-15
 ; Sequence 15, Application US/10282162
 ; Patent No. 6927044
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 ; FILE REFERENCE: REG 203-B-US
 ; CURRENT APPLICATION NUMBER: US/10/282,162
 ; CURRENT FILING DATE: 2002-10-28
 ; PRIOR APPLICATION NUMBER: 09/787,835
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/US99/22045
 ; PRIOR FILING DATE: 1999-09-22
 ; NUMBER OF SEQ ID NOS: 56
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-282-162-15

Query Match 66.8%; Score 1910; DB 2; Length 360;
 Best Local Similarity 99.4%; Pred. No. 3.2e-150;
 Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 DB 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 QY 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344
 DB 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344

RESULT 10
 5171840-7
 ; Patent No. 5171840
 ; APPLICANT: KISHIMOTO, TADAMITSU
 ; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
 ; STIMULATORY FACTOR-2
 ; NUMBER OF SEQUENCES: 11
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/298,694
 ; FILING DATE: 19-JAN-1989
 ; SEQ ID NO: 7;
 ; LENGTH: 344
 5171840-7

Query Match 64.7%; Score 1852; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-145;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 DB 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 QY 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344
 DB 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344

RESULT 11
 5480796-7
 ; Patent No. 5480796
 ; APPLICANT: KISHIMOTO, TADAMITSU
 ; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
 ; FOR HUMAN B CELL STIMULATORY FACTOR-2
 ; NUMBER OF SEQUENCES: 8
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/907,650
 ; FILING DATE: 02-JUL-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 298,694
 ; FILING DATE: 19-JAN-1989
 ; SEQ ID NO: 7;
 ; LENGTH: 344
 5480796-7

Query Match 64.7%; Score 1852; DB 7; Length 344;
 Best Local Similarity 100.0%; Pred. No. 2e-145;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 DB 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESOKFSCQLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGCIGLQDPPANITVTAVARNRWLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHDAWSGLRHVVQLRAQBEFGQ 300
 QY 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344
 DB 301 GEMSEWSPAMGTPMTESRSPPAENEVSTPMQALTTNKDDNIL 344

RESULT 12
 US-09-313-942-26
 ; Sequence 26, Application US/09313942
 ; Patent No. 6472179
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.

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; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

Query Match      62.5%; Score 1788; DB 2; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.5e-139;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRRLRLRSVLQHDGNSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||

QY 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
   :|||||

QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQAL 334
   :|||||
Db 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMELL 334
   :|||||

RESULT 13
US-10-282-162-26
; Sequence 26, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-26

Query Match      62.5%; Score 1788; DB 2; Length 1158;
Best Local Similarity 99.1%; Pred. No. 2.5e-139;
Matches 331; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRRLRLRSVLQHDGNSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPPAAGSHPSRWAGMGRRLRLRSVLQHDGNSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||

QY 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
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QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQAL 334
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Db 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMELL 334
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RESULT 14
US-09-313-942-24
; Sequence 24, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-24

Query Match      62.3%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 6.6e-139;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||
Db 1 MVAVGCCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
   :|||||

QY 61 VLKPPAAGSHPSRWAGMGRRLRLRSVLQHDGNSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||
Db 61 VLKPPAAGSHPSRWAGMGRRLRLRSVLQHDGNSCYRAGRPACTVHLLVDVPPPEPQLS 120
   :|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEQCOYSQESKFSQCLAV 180
   :|||||

QY 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||
Db 181 PEGDSSFFIIVSMCVASSVSGSKFTQTFQCGGILQPDPPANITVTAVARNRWLSVTWQD 240
   :|||||

QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
   :|||||
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEBFGQ 300
   :|||||

QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPM 331
   :|||||
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Db 301 GEWSESPAMGTPWTEGRSPPAENEVSTPM 331

RESULT 15
US-10-282-162-24
; Sequence 24, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-24

Query Match 62.3%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 6.6e-139;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MVAVGCALLAALLAAPGALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVGSKFSTQTFQCGILOPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVGSKFSTQTFQCGILOPDPANITVTAVARNPRWLSVTWQD 240

QY 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGRLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGRLRHVVQLRAQEEFGQ 300

QY 301 GEWSESPAMGTPWTEGRSPPAENEVSTPM 331
Db 301 GEWSESPAMGTPWTEGRSPPAENEVSTPM 331

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Job time : 51 secs

11/11/11

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:30:56 ; Search time 181 Seconds
(without alignments)
1389.645 Million cell updates/sec

Title: US-09-462-416A-7
Perfect score: 2861
Sequence: 1 MLAVGCALLAALLAAGPAAAL.....LILRSFKFLOSLRALRQM 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2772	96.9	569	5	US-10-485-545A-14
2	1921	67.1	592	3	US-09-313-942-8
3	1921	67.1	592	3	US-09-313-942-8
4	1921	67.1	592	4	US-09-935-868-8
5	1921	67.1	592	4	US-10-287-035-8
6	1921	67.1	592	4	US-10-282-162-8
7	1918	67.0	468	4	US-11-134-114-8
8	1918	67.0	468	5	US-10-247-463-12
9	1918	67.0	468	6	US-10-756-149-5377
10	1910	66.8	360	3	US-09-313-942-15
11	1910	66.8	360	3	US-09-935-868-15
12	1910	66.8	360	4	US-10-287-035-15
13	1910	66.8	360	4	US-10-282-162-15
14	1910	66.8	360	6	US-11-134-114-15
15	1902	66.5	468	5	US-10-485-545A-11
16	1897	66.3	357	5	US-10-485-545A-13
17	1891	66.1	364	5	US-10-485-545A-10
18	1891	66.1	365	5	US-10-485-545A-12
19	1823.5	63.7	453	4	US-10-322-696-14
20	1788	62.5	1158	3	US-09-313-942-26
21	1788	62.5	1158	3	US-09-935-868-26
22	1788	62.5	1158	4	US-10-287-035-26
23	1788	62.5	1158	4	US-10-282-162-26
24	1788	62.5	1158	6	US-11-134-114-26
25	1783	62.3	1168	3	US-09-313-942-24
26	1783	62.3	1168	3	US-09-935-868-24
27	1783	62.3	1168	4	US-10-287-035-24

28	1783	62.3	1168	4	US-10-282-162-24	Sequence 24, Appl
29	1783	62.3	1168	6	US-11-134-114-24	Sequence 24, Appl
30	1683	58.8	315	3	US-09-313-942-16	Sequence 16, Appl
31	1683	58.8	315	3	US-09-935-868-16	Sequence 16, Appl
32	1683	58.8	315	4	US-10-287-035-16	Sequence 16, Appl
33	1683	58.8	315	4	US-10-282-162-16	Sequence 16, Appl
34	1683	58.8	315	6	US-11-134-114-16	Sequence 16, Appl
35	954.5	33.4	387	4	US-10-322-696-141	Sequence 141, Appl
36	954.5	33.4	460	4	US-10-247-463-13	Sequence 13, Appl
37	954.5	33.4	460	6	US-11-016-106-13	Sequence 13, Appl
38	939.5	32.8	266	6	US-11-043-788-194	Sequence 194, Appl
39	938.5	32.8	212	3	US-09-854-280-14	Sequence 14, Appl
40	938.5	32.8	212	3	US-09-854-208-14	Sequence 14, Appl
41	938.5	32.8	212	4	US-10-099-007A-3	Sequence 3, Appl
42	938.5	32.8	212	4	US-10-400-377-13	Sequence 13, Appl
43	938.5	32.8	212	4	US-10-400-708-13	Sequence 13, Appl
44	938.5	32.8	212	4	US-10-298-148-13	Sequence 13, Appl
45	938.5	32.8	212	4	US-10-440-464-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-485-545A-14
; Sequence 14, Application US/10485545A
; Publication No. US20050064558A1
; GENERAL INFORMATION:
; APPLICANT: University College Cardiff
; APPLICANT: University of Wales College of Medicine
; TITLE OF INVENTION: A Fusion Protein
; FILE REFERENCE: P102803PCT
; CURRENT APPLICATION NUMBER: US/10/485,545A
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: 0119015.6
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 14
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-6 fusion protein
US-10-485-545A-14

Query Match		96.9%	Score 2772;	DB 5;	Length 569;
Best Local Similarity		95.4%	Pred. No. 2.2e-206;		
Matches 535;		Conservative 0;	Mismatches 6;	Indels 20;	Gaps 3;
QY	1	MLAVGCALLAALLAAGPAAALPRRC	PAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60	
DB	1	MLAVGCALLAALLAAGPAAALPRRC	PAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60	
QY	61	VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDS	GNYSYCYRAGRPAGTVHLVLDVPPPEPQLS	120	
DB	61	VLRKPAAGSHPSRWAGMGRLLRLRSVQLHDS	GNYSYCYRAGRPAGTVHLVLDVPPPEPQLS	120	
QY	121	CFRKPSPLNVCEWGPSTPSLT	TKAVLLVRKFSQSPADFPQCYSESQKFSQCLAV	180	
DB	121	CFRKPSPLNVCEWGPSTPSLT	TKAVLLVRKFSQSPADFPQCYSESQKFSQCLAV	180	
QY	181	PGDSSFFYIVSMCVASSVGS	KFTQTFQCGILOPPANTITVTAVARNPRLSVTWOD	240	
DB	181	PGDSSFFYIVSMCVASSVGS	KFTQTFQCGILOPPANTITVTAVARNPRLSVTWOD	240	
QY	241	PHSMNSSFYRLRFELRYAERS	SKTFTTWVKDLQHCVTHDAWSGLRHVVQLRAQEFQ	300	
DB	241	PHSMNSSFYRLRFELRYAERS	SKTFTTWVKDLQHCVTHDAWSGLRHVVQLRAQEFQ	300	
QY	301	GWSEWSPEAMGTPWTESR	PPPAENVEVSTPMQALTTNKDDNILLFRDSANATSLP	355	
DB	301	GWSEWSPEAMGTPWTESR	PPPAENVEVSTPMQALTTNKDDNILLFRDSANATSLP	355	


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; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-8
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Query Match 67.1%; Score 1921; DB 6; Length 592;

Best Local Similarity 77.1%; Pred. No. 3.1e-140;

Matches 377; Conservative 22; Mismatches 44; Indels 46; Gaps 5;

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Qy 1 MLAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQPCQYSQESQKFCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQPCQYSQESQKFCQLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQPPANNITTVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQPPANNITTVARNPRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
Qy 301 GESEWSPGAMGTPTWTSRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db 301 GESEWSPGAMGTPTWTSRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Qy 361 VPPGEDSKDVAAPRQPLTSSERIDKQIRYILDGIALRKETCKNSMCE--SSKEALAE 418
Db 358 -----DAGEP-----KSCDKTHTCPCPAPELGG 382
Qy 419 NLNLAKMAEKGCGFCQGFNEETCLVKIIT--GLLEFEVYLEVQ--NRFESSEQAR 472
Db 383 PSVFLFPPKPKDTLMISRTPEVTCVVDSVSHEDPEVFNWYVDGVFNNAKTRPRRQYN 442
Qy 473 AVQMSTKVL 481
Db 443 STYRVSVVL 451
RESULT 7
US-10-247-463-12
; Sequence 12, Application US/10247463
; Publication No. US20030082734A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: DX09920
; CURRENT APPLICATION NUMBER: US/10/247,463
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 468
; TYPE: PRT
; ORGANISM: primate
US-10-247-463-12
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Query Match 67.0%; Score 1918; DB 4; Length 468;

Best Local Similarity 96.5%; Pred. No. 3.8e-140;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

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Qy 1 MLAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQPCQYSQESQKFCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQPCQYSQESQKFCQLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQPPANNITTVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQPPANNITTVARNPRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVHIDAWSGLRHVVQLRAQEEFGQ 300
Qy 301 GESEWSPGAMGTPTWTSRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db 301 GESEWSPGAMGTPTWTSRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Qy 361 VPPGEDSKDVAAP 373
Db 357 -----QDSSSVPLP 365
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RESULT 8

US-10-756-149-5377

; Sequence 5377, Application US/10756149

; Publication No. US20050181375A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS A

; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER

; FILE REFERENCE: file

; CURRENT APPLICATION NUMBER: US/10/756,149

; CURRENT FILING DATE: 2004-01-12

; NUMBER OF SEQ ID NOS: 5818

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5377

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-756-149-5377

Query Match 67.0%; Score 1918; DB 5; Length 468;

Best Local Similarity 96.5%; Pred. No. 3.8e-140;

Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

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Qy 1 MLAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAALPAAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNVSCYRAGPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQPCQYSQESQKFCQLAV 180
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Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPV---- 356
QY 361 VPPGEDSKDVAAP 373
Db 357 ----QDSSSVPLP 365
RESULT 9
US-11-016-106-12
; Sequence 12, Application US/11016106
; Publication No. US20050106673A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: DX09920
; CURRENT APPLICATION NUMBER: US/11/016,106
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 468
; TYPE: PRT
; ORGANISM: primate
US-11-016-106-12
Query Match 67.0%; Score 1918; DB 6; Length 468;
Best Local Similarity 96.5%; Pred. No. 3.8e-140;
Matches 360; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPVEFMP 360
Db 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPV---- 356

QY 361 VPPGEDSKDVAAP 373
Db 357 ----QDSSSVPLP 365
RESULT 10
US-09-313-942-15
; Sequence 15, Application US/093113942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-15
Query Match 66.8%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTRKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQCLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKTQTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVHDAWSGLRHVVQLRAQEEFGQ 300
QY 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357
Db 301 GWSWSPEAMGTPMTESRSPAEENEVSTPMQALTTNKDDNILFRDSANATSLPVQ 357
RESULT 11
US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 360

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match          66.8%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300

Qy 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 12
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: NEIL STAHL AND GEORGE D. YANCOPOULOS
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match          66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300

Qy 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 13
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-15

Query Match          66.8%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGNSYCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKESCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300
Db 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHCVCVIHDAWSGLRHVVQLRAQEFQG 300

Qy 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357
Db 301 GEWSEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVE 357

RESULT 14
US-11-134-114-15
; Sequence 15, Application US/11134114
```

Publication No. US20050222033A1
GENERAL INFORMATION:
APPLICANT: Stahl, Neil
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
FILE REFERENCE: 203C1
CURRENT APPLICATION NUMBER: US/11/134,114
PRIOR FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: 10/282,162
PRIOR FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-11-134-114-15

Query Match 66.8%; Score 1910; DB 6; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-139;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPPPEPOLS 120
DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPPPEPOLS 120
QY 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESKFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
QY 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
DB 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVE 357
DB 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVE 357

RESULT 15
US-10-485-545A-11
Sequence 11, Application US/10485545A
Publication No. US20050064558A1
GENERAL INFORMATION:
APPLICANT: University College Cardiff
TITLE OF INVENTION: A Fusion Protein
FILE REFERENCE: P102803PCT
CURRENT APPLICATION NUMBER: US/10/485,545A
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: 0119015.6
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: SeqWin99, version 1.02
SEQ ID NO 11
LENGTH: 468
TYPE: PRT

ORGANISM: homo sapien
US-10-485-545A-11
Query Match 66.5%; Score 1902; DB 5; Length 468;
Best Local Similarity 96.0%; Pred. No. 6.7e-139;
Matches 358; Conservative 1; Mismatches 6; Indels 8; Gaps 1;
QY 1⁴ MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPPPEPOLS 120
DB 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPPPEPOLS 120
QY 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESKFSCQLAV 180
QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVTAVARNRWLSVTWQD 240
QY 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
DB 241 PHSWNSSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVQLRAQEEFGQ 300
QY 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVE 360
DB 301 GEWSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVE 360
QY 361 VPPGEDSKDVAAP 373
DB 357 ----QDSSSVPLP 365

Search completed: September 7, 2006, 23:34:34
Job time : 182 secs

1. The first part of the document is a list of names and titles, including "The Hon. Mr. Justice" and "The Hon. Mr. Justice".

|||||
Db 117 CFRKSPNVCVWGFRSTPISLTTKAVLLVRKFQNSPAEDFQBPQCQSQBSQKSCQAV 176
Qy 181 PEGDSSFIVSMCVASSVGSFKSTQTQTFQGGGILQPDPPANITVTAVARNRWLSVTWQD 240
Db 177 PEGDSSFIVSMCVASSVGSFKSTQTQTFQGGGILQPDPPANITVTAVARNRWLSVTWQD 236
Qy 241 PHSWNSSRYRLRFELRYAERSKTFTTMMVKDLQHCCHVHDWGLRHVVQLRAQEFQG 300
Db 237 PHSWNSSRYRLRFELRYAERSKTFTTMMVKDLQHCCHVHDWGLRHVVQLRAQEFQG 296
Qy 301 GEWSEWSPGAGTPTWESRSPPAENEVSTPMQALTTNNKDDNILLFRSANATSLPVEFMP 360
Db 297 GEWSEWSPGAGTPTWESRSPPAENEVSTPMQALTTNNKDDNILLFRSANATSLPV---- 352
Qy 361 VPPGEDSKDVAAP 373
Db 353 ----QDSSSVPLP 361

RESULT 2
US-10-505-928-453
; Sequence 453, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 453
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-453

Query Match 32.8%; Score 938.5; DB 6; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-61;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
Db 22 LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
Qy 413 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 472
Db 82 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 141
Qy 473 AVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQNLQDMTTHLILRSKF 532
Db 142 AVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQNLQDMTTHLILRSKF 201
Qy 533 LQSSLRALROM 543
Db 202 LQSSLRALROM 212

RESULT 3
US-10-511-937-2489
; Sequence 2489, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald

4
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2489
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2489

Query Match 32.8%; Score 938.5; DB 6; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-61;
Matches 187; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
Qy 354 LPVEF-MPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 412
Db 22 LPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNMCESS 81
Qy 413 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 472
Db 82 KEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLEYLQNRFSSEBOAR 141
Qy 473 AVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQNLQDMTTHLILRSKF 532
Db 142 AVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQNLQDMTTHLILRSKF 201
Qy 533 LQSSLRALROM 543
Db 202 LQSSLRALROM 212

RESULT 4
US-10-933-854-11
; Sequence 11, Application US/10933854
; Publication No. US20060105347A1
; GENERAL INFORMATION:
; APPLICANT: GTC Biotherapeutics, Inc.
; APPLICANT: Meade, Harry
; APPLICANT: Cox, Geoffrey F.
; TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammals
; FILE REFERENCE: GTC-220 PCT
; CURRENT APPLICATION NUMBER: US/10/933,854
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/500,910
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Human a Interferon Variant 2A
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/EMBL/DBJ Accession No. CAA00839
; DATABASE ENTRY DATE: 1993-12-03
; RELEVANT RESIDUES: (1)..(212)
US-10-933-854-11

Query Match 32.8%; Score 938.5; DB 6; Length 212;
Best Local Similarity 97.9%; Pred. No. 1.5e-61;

Matches	187;	Conservative	0;	Mismatches	3;	Indels	1;	Gaps	1;
Qy	354	LPVEF-MPVPPGEDSKDVAAPHROPLTSSSRIDKQIRYILDGISALRKETCNKNMCESS	412						
Db	22	LPAAFPAPVPPGEDSKDVAAPHROPLTSSSRIDKQIRYILDGISALRKETCNKNMCESS	81						
Qy	413	KEALAENNLNPKMAEKDGCFOSGFNSETCLVKIITGLLEPEVLYEVLONPFESSEQAR	472						
Db	82	KEALAENNLNPKMAEKDGCFOSGFNSETCLVKIITGLLEPEVLYEVLONPFESSEQAR	141						
Qy	473	AVOMSTKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQAQONQLQDMTTHLIIRSPKEF	532						
Db	142	AVOMSTKVLQFLOKKAKNLDAITTPDPTTNASLLTKLQAQONQLQDMTTHLIIRSPKEF	201						
Qy	533	LOSSLRALRQM	543						
Db	202	LOSSLRALROM	212						

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RESULT 5
US-11-330-917-198
; Sequence 198, Application US/11330917
; Publication No. US20060182716A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Jin
; APPLICANT: Seiwert, Scott D.
; APPLICANT: Blatt, Lawrence M.
; TITLE OF INVENTION: Synthetic Hyperglycosylated, Protease-Resistant Polypeptide Variants
; TITLE OF INVENTION: Oral Formulations and Methods of Using the Same
; FILE REFERENCE: INTM-060W0
; CURRENT APPLICATION NUMBER: US/11/330,917
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 60/600,202
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/600,134
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/604,280
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/604,415
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 1354
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-330-917-198

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RESULT 6
US-10-669-920-1402
; Sequence 1402, Application US/10669920
; Publication No. US20060194265A1

```

; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1402
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
; UN-10-669-920-1402

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RESULT 7
US-10-669-920-1405
; Sequence 1405, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001

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; CURRENT APPLICATION NUMBER: US/10/569,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-669-920-1405

Query Match      31.7%; Score 908; DB 6; Length 277;
Best Local Similarity 92.9%; Pred. No. 3.6e-59;
Matches 169; Conservative 1; Mismatches 4; Indels 8; Gaps 1;

Qy 192 MCVASSVGSKFSKTKTQGGCIGLOPPANITVTAVARNPRLSVTWQDPHSMNSFYRL 251
Db 1 MCVASSVGSKFSKTKTQGGCIGLOPPANITVTAVARNPRLSVTWQDPHSMNSFYRL 60

Qy 252 RFELRYRAERSKTFTHVMVKDQHCYVHDWSGLRHVVQLRAQEEFGQGEWSPEAM 311
Db 61 RFELRYRAERSKTFTHVMVKDQHCYVHDWSGLRHVVQLRAQEEFGQGEWSPEAM 120

Qy 312 GTPWTSRSPPAENEVSTPMQALTNKDDNILFRDSANATSLPVEFMPVPVPGDSDKVA 371
Db 121 GTPWTSRSPPAENEVSTPMQALTNKDDNILFRDSANATSLPVEFMPVPVPGDSDKVA 172

Qy 372 AP 373
Db 173 LP 174

RESULT 8
; Sequence 38075, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38075
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-38075

Query Match      10.6%; Score 303; DB 6; Length 368;
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Best Local Similarity 28.4%; Pred. No. 1.3e-14;
Matches 108; Conservative 44; Mismatches 148; Indels 80; Gaps 17;

Qy 12 LLAAPGAALAPRCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWLRLKPAAGSHP 71
Db 12 LLAAGVVAYQRH---SQDTHVLYERLGSVDVILPC-GTAAWGTAVTWVNGTDLBAHY 67

Qy 72 SRWAGMRLLRLSRVQLHDSGNYSYCRAG---RPAGTVHLLVDVPPPEPQLSCFRKSPL 127
Db 68 N-----GSQVLVEGLDLSHSGHYACVGGSSWHLRYQALLH--VGMPPREPVLTCRSNSYP 120

Qy 128 SNVVCW---GPRSTPSLTITKAVLLVRKP---QNSPAEDFQEPQCISQESQKESCOLAVP 181
Db 121 KGFYCSWHLPSPTFIPTNFVTVLHGSKLLGCKEOPA-----PKNRCHIRYT 167

Qy 182 EGDSSF-YIVSMCVASSVGSKFSKTKTQGGCIGLOPPANITVTAVARNPRLSVTWQD 240
Db 168 HLFSTVKYKVTLVITNALGHN-STAITFDEFTIVKPPDENVAVRPPVSSPRRLEVTWQT 226

Qy 241 PHSW-NSSFYRLRFELRYRAERSKTFTHVMVKDQHC-----VIHDAWSGLRHVVQ 291
Db 227 PSSWPDPESPPLKFFLYRP-----LILDQWQHVELSDGTTHTITDAYAGKEYIIQ 277

Qy 292 LRAQEEFGQGEWSPEAMGTPTWTSRSPPAENEVSTPMQALTNKDDNILFRDSANA 351
Db 278 VAAKDN-EIGTWSDSVVAHAHATPTEE-----PRYLTTEAQAPET-----T 317

Qy 352 TSLPVEFMPVP-----PGE 365
Db 318 TTTTTFVFPPTTKICDPGE 337

RESULT 9
US-11-296-092-32
; Sequence 32, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
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; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-296-092-32

Query Match          7.0%; Score 201; DB 7; Length 422;
Best Local Similarity 24.7%; Pred. No. 4.6e-07;
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

QY 8 LLAALLAAGA-----ALAPRCFAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWV 61
DB 24 LLLCVLGAPRAGSGAHTAVISQDP-----TLIGSSLLATC-----SVHG- 64
QY 62 LRKPAAGSHPSRWAGMGRLL-----LLRSVQLHDSGNYSCY-RAGRP 102
DB 65 -DPPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSI 123
QY 103 AGTVHLLVDVPPPEP-QLSCFRKSPLSNVVCEWGP-----RSTPSLTTKAVLLVRKF 153
DB 124 LAGSCLYVGLPEKPVNISCSKN-MKDLTCRWTPGAHGETFLHTNYSLYK-----LRWY 178
QY 154 -QNSPAEDFQBPQCOYSQBSQKFSQCLAVPEGDSSF--YIVSMCVASSVGSKFSKTQTQFG 210
DB 179 QDNTCEEYHTVGPH-----SCH--IPKDLALFTPYEIVWEATNRLGSARSDVLTLDI 229
QY 211 CGILQDPPANITVTAVARNPRWLSVTWQDPHSMNSPYRLRFLRYRAERSKTFITTMV 270
DB 230 LDVVTDDPPDVHVSRRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDS---VDMKV 286
QY 271 KD---LQHCVTIDAWSGRLRHVVQLRAQEEFG-----QGEWSEWS-PEAMGTPWTESRS 320
DB 287 VDDVSNQTSCLAGLKPGTVFVQVRC-NPFGIYSGKAGIWESEHPTAASTPRSRPG 345
QY 321 P-----PAENEVSTPMQALTNNKDDNILFR 346
DB 346 PGGACEPRGPGSPGVRRELKQFLGWLKKHAYCSNLSFR 386

RESULT 10
US-11-296-155-32
; Sequence 32, Application US/11296155
; Publication No. US20060127983A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: US/11/296,155
; CURRENT FILING DATE: 2005-12-06
; PRIOR APPLICATION NUMBER: US/09/866,028
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-296-155-32

Query Match          7.0%; Score 201; DB 7; Length 422;
Best Local Similarity 24.7%; Pred. No. 4.6e-07;
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

QY 8 LLAALLAAGA-----ALAPRCFAQVARGVLTSLPGDSVTLTCGVEPEDNATVHWV 61
DB 24 LLLCVLGAPRAGSGAHTAVISQDP-----TLIGSSLLATC-----SVHG- 64
QY 62 LRKPAAGSHPSRWAGMGRLL-----LLRSVQLHDSGNYSCY-RAGRP 102
DB 65 -DPPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSI 123
QY 103 AGTVHLLVDVPPPEP-QLSCFRKSPLSNVVCEWGP-----RSTPSLTTKAVLLVRKF 153
DB 124 LAGSCLYVGLPEKPVNISCSKN-MKDLTCRWTPGAHGETFLHTNYSLYK-----LRWY 178
QY 154 -QNSPAEDFQBPQCOYSQBSQKFSQCLAVPEGDSSF--YIVSMCVASSVGSKFSKTQTQFG 210
DB 179 QDNTCEEYHTVGPH-----SCH--IPKDLALFTPYEIVWEATNRLGSARSDVLTLDI 229
QY 211 CGILQDPPANITVTAVARNPRWLSVTWQDPHSMNSPYRLRFLRYRAERSKTFITTMV 270
DB 230 LDVVTDDPPDVHVSRRVGGLEDQLSVRWSPPALKDFLFOAKYQIRYRVEDS---VDMKV 286
QY 271 KD---LQHCVTIDAWSGRLRHVVQLRAQEEFG-----QGEWSEWS-PEAMGTPWTESRS 320
DB 287 VDDVSNQTSCLAGLKPGTVFVQVRC-NPFGIYSGKAGIWESEHPTAASTPRSRPG 345
QY 321 P-----PAENEVSTPMQALTNNKDDNILFR 346
DB 346 PGGACEPRGPGSPGVRRELKQFLGWLKKHAYCSNLSFR 386

RESULT 11
US-11-300-928-27
; Sequence 27, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
; APPLICANT: Karumanchi, S. Ananth
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treati
; TITLE OF INVENTION: Complications of Pregnancy
; FILE REFERENCE: 01948/108002
; CURRENT APPLICATION NUMBER: US/11/300,928
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US 60/636,275
```


Qy 325 NE-----VSTPMQA-----LITNKDD----- 341
 Db 341 TQGYRTVQLVWTKLTPPPPEANGKILDYEVTLTRWKSHLQNYTVNATKLTVNLTDYRYLATL 400
 Qy 342 ---NLPFDSANATSLPV-EMPVPPGSDSDVAAPHQPL-----TSSEIDKQIRVIL 392
 Db 401 TVRLVGVGSDAAVUTIPACDFQATHPVMDLK--APPKONMLWVEWTTTPRESVKK---YIL 455
 Qy 393 DGISALRKETC 403
 Db 456 EMCVLSDKAPC 466

RESULT 14
 US-11-234-676-321
 ; Sequence 321, Application US/11234676
 ; Publication No. US20060193921A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cload, Sharon T.
 ; APPLICANT: Diener, John L.
 ; APPLICANT: Ferguson, Alicia
 ; APPLICANT: Hamaguchi, Nobuko
 ; APPLICANT: Keene, Sara C.
 ; APPLICANT: Lagasse, H.A. Daniel
 ; APPLICANT: Sawhney, Pooja
 ; APPLICANT: Thompson, Kristin
 ; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
 ; TITLE OF INVENTION: Autoimmune Disease Therapeutics
 ; FILE REFERENCE: 23239-578 CIP
 ; CURRENT APPLICATION NUMBER: US/11/234,676
 ; CURRENT FILING DATE: 2005-09-22
 ; PRIOR APPLICATION NUMBER: 11/075,649
 ; PRIOR FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: 60/550,962
 ; PRIOR FILING DATE: 2004-03-05
 ; PRIOR APPLICATION NUMBER: 60/608,046
 ; PRIOR FILING DATE: 2004-09-07
 ; NUMBER OF SEQ ID NOS: 323
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 321
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-11-234-676-321

Query Match 5.5%; Score 158.5; DB 7; Length 335;
 Best Local Similarity 21.1%; Pred. No. 0.00044;
 Matches 68; Conservative 51; Mismatches 113; Indels 91; Gaps 15;
 Qy 39 PGDSVTLTCGVEPEDNATVHW--LRKPAAGSHPSRWAGMGRLLRLRSVOLHDSGNYS 96
 Db 42 PGETVNLTCDTPEEDD-----ITWTSQRHGVIGS-----GKTUTITVKEFLDAGQYTC 90
 Qy 97 YRAGRAGTAVHLLVDVP-----PEEPOLSCFRKSPLSNVVCEW----- 134
 Db 91 HKGETLHSHLLHKKENGIGWSTEILKNFKNFKLCEAPNYSGRFTCSMLVQRNMDLK 150
 Qy 135 ---GPRSTP-----SLTTKAVLLVRKFNQSPAEQPCQYQSQKFSQ--L 178
 Db 151 FNIKSSSSSPDSRAVTCGMASLSAEKVTL-----DQDYEKYSVSCQEDV 195
 Qy 179 AVPEGDSSFYIVSMCVASSVSGSKFSTOT-FQCGGILQDPANITVTAVARNPRLSVT 237
 Db 196 TCPTAEETLPI-ELALEARQONKYNYSFTFIRDIIRPDPPKNLQMKPLKNSQ--VEVS 252
 Qy 238 WODPHSWNS--SFYRLRFLRYRABRSKTFITTMVKDLQHHCVIHDW-----S 284
 Db 253 WEYPDSTPHSYFSLKFFVRLQRKEK-----MKETECCNQKGAFLVEKSTEVQCK 306
 Qy 285 GLRHVVQLRAQBEFGCGWSEWS 307
 Db 307 GGNVCVQ--AQDRYNNSSCSKWA 327

RESULT 15
 US-10-669-920-93
 ; Sequence 93, Application US/10669920
 ; Publication No. US20060194265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Malandro, Marc S.
 ; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
 ; FILE REFERENCE: 20366-066001
 ; CURRENT APPLICATION NUMBER: US/10/669,920
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: US 10/004,113
 ; PRIOR FILING DATE: 2001-10-23
 ; PRIOR APPLICATION NUMBER: US 10/052,482
 ; PRIOR FILING DATE: 2001-11-08
 ; PRIOR APPLICATION NUMBER: US 09/997,722
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 10/034,650
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 10/085,117
 ; PRIOR FILING DATE: 2002-02-27
 ; PRIOR APPLICATION NUMBER: US 10/087,192
 ; PRIOR FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 10/322,281
 ; PRIOR FILING DATE: 2002-12-17
 ; PRIOR APPLICATION NUMBER: US 10/322,696
 ; PRIOR FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 1441
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 93
 ; LENGTH: 306
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-669-920-93

Query Match 5.4%; Score 155; DB 6; Length 306;
 Best Local Similarity 22.6%; Pred. No. 0.00071;
 Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;
 Qy 113 PPEPOLSCFRKSPLSNVVCEWGRSTPSLTTKAVLLVRKFNQSPAEQPCQYQSQ 172
 Db 20 PPGKPEITHKCRSPDKETFTTCWNPBGDGLPTNYSL-----TYSKEGE 62
 Qy 173 K--FSCQLAVPEGDSS-----FYIVSMCVASSVSGSKFSTOTFQCGGILQDP 218
 Db 63 KNTCEPDYKTSGNPSCFFSKQYTSIKWYIITVNTATNMGSSSTDPLYVDVYIVEPEP 122
 Qy 219^aPANIT--VTAVARNPRLSVTWQDP--HSWNSSFYRLRFLRYRABRSKTFITTMVKDLQ 274
 Db 123 PRNLTLEVKQLDKKTYLWVKWLPPTITDVKTGWFTMEYIRLKSEEA---DEWEIHFTG 179
 Qy 275 HHC--VIHDAMSLRHVVQLRAQBEFGCGWSEWSPE 309
 Db 180 HQTOFKVPDLYPGQKYLQVTRCKPD--HGYWSRMQGE 214

Search completed: September 7, 2006, 23:35:13
 Job time : 35 secs

10-11-1971

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 22:54:31 ; Search time 193 Seconds
(without alignments)
1310.055 Million cell updates/sec

Title: US-09-462-416a-13

Perfect score: 2912
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILSRKPEFLQSSLRALRQM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2846	97.7	543	2	AA03164 Chimeric
2	2786.5	95.7	570	6	ABP72702 Human int
3	2661	91.4	525	2	AAW36846 Human fus
4	2658.5	91.3	515	3	AAB15404 IL-6R/IL-
5	2527.5	86.8	500	2	AAW36847 Human fus
6	2144.5	73.6	419	2	AAW30938 Human IL-
7	1929	66.2	690	3	AAW92195 Human IL-
8	1927.5	66.2	592	2	AAW70797 Human int
9	1927.5	66.2	592	3	AAW92185 Human IL-
10	1927.5	66.2	592	7	ABW02165 Human IL-
11	1923.5	66.1	468	3	AAW92196 Human IL-
12	1922	66.0	477	3	AAW92197 Human IL-
13	1917	65.8	468	1	AAW90284 Sequence
14	1917	65.8	468	2	AAW92185 Human IL-
15	1917	65.8	468	4	AAW36655 Human IL-
16	1917	65.8	468	5	AAW28593 Interleuk
17	1917	65.8	468	5	ABB78191 Amino aci
18	1917	65.8	468	6	ABP72697 Human int
19	1917	65.8	468	7	ADC07187 Human int
20	1917	65.8	468	8	ADP54591 Human PRO
21	1917	65.8	468	8	ADP23941 PRO polyp
22	1917	65.8	468	9	ADZ13887 Human can
23	1917	65.8	468	9	ADZ25538 Human IL-

24	1917	65.8	468	9	ADZ65022 Human IL-
25	1917	65.8	468	9	AED08341 Amino aci
26	1917	65.8	468	9	AED96935 Human C-r
27	1914	65.7	365	9	AED65387 Human int
28	1914	65.7	468	2	AAW98364 Interleuk
29	1913	65.7	357	6	ABP72699 Soluble i
30	1910	65.6	360	2	AAW70804 Amino aci
31	1910	65.6	360	3	AAW92199 Soluble h
32	1910	65.6	360	7	ABW02172 Human IL-
33	1909	65.6	468	1	AAW90525 B cell st
34	1907	65.5	364	6	ABP72698 Soluble i
35	1899	65.2	468	2	AAW71371 Human int
36	1891.5	65.0	499	9	AED96936 Human C-r
37	1858	63.8	345	3	AAW55071 SR345 pro
38	1852	63.6	344	1	AAW90528 B cell st
39	1822.5	62.6	453	8	ADQ59508 Human can
40	1791	61.5	384	9	AED96937 Human C-r
41	1789	61.4	1158	3	AAW92205 Fusion po
42	1789	61.4	1158	7	ABW02178 Human cyt
43	1783	61.2	1168	3	AAW92204 Fusion po
44	1783	61.2	1168	7	ABW02177 Human cyt
45	1764	60.6	1042	2	AAW70122 IL8-R typ

ALIGNMENTS

RESULT 1

AA03164 ID AA03164 standard; protein; 543 AA.
XX AC AA03164;
XX DT 11-JUN-1999 (first entry)
XX DE Chimeric sIL-6R/IL-6 protein.
XX KW Soluble interleukin-6 receptor; interleukin-6; sIL-6; IL-6; sIL-6/IL-6;
KW chimeric protein; fusion protein; cell growth inhibitor; melanoma cell;
KW highly malignant cancer cell; in vivo engraftment; mammalian cancer;
KW human haematopoietic cell; bone marrow transplantation; mammalian cancer;
KW hepatotoxic agent protection; haematopoiesis; liver disorder;
KW neurological disorder.
XX OS Synthetic.
XX FN WO9902552-A2.
XX PD 21-JAN-1999.
XX PF 09-JUL-1998; 98WO-IL000321.
XX PR 10-JUL-1997; 97IL-0012184.
XX PR 30-DEC-1997; 97IL-00122818.
XX PA (VEDA) YEDA RES & DEV CO LTD.
XX FI Revel M, Chebath J, Lapidot T, Kollet O;
XX WIPI; 1999-120776/10.
XX PT New glycosylated soluble IL-6 receptor/IL-6 conjugates - used for e.g.
XX PT treating cancers, bone marrow transplantation, increasing haematopoiesis
XX or treating liver or neurological disorders.
XX PS Claim 6; Fig 3; 77pp; English.
XX CC This sequence represents the chimeric glycosylated soluble interleukin-6
CC receptor (sIL-6R)-interleukin-6 (IL-6) protein (sIL-6R/IL-6) of the
CC invention. It comprises a fusion protein product between all of the
CC naturally occurring form of sIL-6R and all of the naturally occurring
CC form of IL-6, the sIL-6/IL-6 and analogues being glycosylated in a
CC similar fashion to the glycosylation of naturally occurring sIL-6R and IL

CC -6. The sIL-6R/IL-6 and analogues are capable of inhibiting the growth of
 CC highly malignant cancer cells, e.g. melanoma cells, eliciting the in vivo
 CC engraftment of human hematopoietic cells in bone marrow transplantation
 CC and protecting liver from hepatotoxic agents. They can be used for the
 CC preparation of a medicament for treating mammalian cancers by way of
 CC inhibition of cancer cells, for enhancement of bone marrow
 CC transplantation by way of eliciting engraftment of human hematopoietic
 CC cells in bone marrow transplantation, for increasing haematopoiesis, for
 CC treating liver or neurological disorders, or in other applications in
 CC which IL-6 or sIL-6R are used
 XX
 XX
 SQ Sequence 543 AA;

Query Match 97.7%; Score 2846; DB 2; Length 543;
 Best Local Similarity 98.2%; Pred. No. 2.3e-187;
 Matches 543; Conservative 0; Mismatches 0; Indels 10; Gaps 1;
 Qy 1 MLAVGCALLAALLAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Db 1 MLAVGCALLAALLAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGVSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGVSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Qy 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKESCOLAV 180
 Db 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKESCOLAV 180
 Qy 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGGCGIQQPDPANITVAVARNPRLSVTWQD 240
 Db 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGGCGIQQPDPANITVAVARNPRLSVTWQD 240
 Qy 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAMSGLRHVQLRAQEFQ 300
 Db 241 PHSWNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAMSGLRHVQLRAQEFQ 300
 Qy 301 GEWSEWPEANGTWTESRSPPAENESTVTPQALITNKDDNIIIFRSANATSLPVEFGA 360
 Db 301 GEWSEWPEANGTWTESRSPPAENESTVTPQALITNKDDNIIIFRSANATSLPVE--- 357
 Qy 361 GLVLGGQPMPPGDESKDVAAHQPLTSSERIDKQIRYLDIGISALRKETCKNSMCE 420
 Db 358 -----FMPVPPGDESKDVAAHQPLTSSERIDKQIRYLDIGISALRKETCKNSMCE 410
 Qy 421 SSKEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRPESEEQ 480
 Db 411 SSKEALAEENNLNPKMAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQNRPESEEQ 470
 Qy 481 ARAVQMSTKVLIQFLOKAKNLDATTPDPTTNASLTITKLOAQNWLDWTHILIRSPK 540
 Db 471 ARAVQMSTKVLIQFLOKAKNLDATTPDPTTNASLTITKLOAQNWLDWTHILIRSPK 530
 Qy 541 EFLOSSLRALRQM 553
 Db 531 EFLOSSLRALRQM 543

RESULT 2
 ABP72702
 ID ABP72702 standard; protein; 570 AA.
 XX
 AC ABP72702;
 XX
 DT 11-JUN-2003 (first entry)
 XX
 DE Human interleukin-6-receptor isoform DS-sIL-6R fusion protein.
 XX
 KW Human; interleukin-6; receptor; DS-sIL-6R; antibacterial; virucide;
 KW anti-HIV; antirheumatic; antiarthritic; antiinflammatory;
 KW immunosuppressive; gene therapy.
 XX
 OS Homo sapiens.

OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 XX Protein 1..364
 FT /label= DS-sIL-6R
 FT Peptide 365..376
 FT /label= Linker
 FT Protein 377..560
 FT /label= IL-6
 FT Peptide 561..570
 FT /label= C-myc tag
 XX
 XX WO2003014359-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 02-AUG-2002; 2002WO-GB003581.
 XX
 XX 03-AUG-2001; 2001GB-00019015.
 XX
 XX (UYCA-) UNIV COLLEGE CARDIFF.
 XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 XX Jones SA, Topley N;
 XX
 XX WPI, 2003-256588/25.
 XX
 XX New fusion protein having a functional IL-6 and DS-sIL-6R molecule,
 XX useful for the manufacture of a medicament for the prophylaxis or
 XX treatment of an infectious disease, and an inflammatory or immunological
 XX disorder.

Disclosure; Fig 5; 46pp; English.

The present sequence is the protein sequence of a novel fusion protein comprising a soluble form of the human interleukin-6 receptor, denoted DS-sIL-6R (see also ABP72658), joined via a peptide linker to a human IL-6 molecule (see also ABP72700), with a C-terminal c-myc tag sequence. Administration of this fusion protein results in the increased expression of one or more of MIP-1alpha, MIP-1beta, RANTES or IP-10. High levels of MIP-1alpha, MIP-1beta and RANTES complete with HIV for binding to CCR5 and effectively suppress HIV entry. The fusion protein can be used in the treatment of any disease in which the infectious agent binds to CCR5, especially M-trophic strains of HIV. The invention also provides a nucleic acid molecule encoding the fusion protein, an expression vector, a host cell, and a method of producing the fusion protein in the host cell. The fusion protein, nucleic acid or vector can be used in the manufacture of a medicament for the prophylaxis or treatment of an infectious disease (especially AIDS caused by a M-trophic strain of HIV, or bacterial peritonitis), an inflammatory disorder or an immunological disorder (especially rheumatoid arthritis), when it is desirable to increase or resolve an immune response (claimed)

Sequence 570 AA;

Query Match 95.7%; Score 2786.5; DB 6; Length 570;
 Best Local Similarity 96.1%; Pred. No. 3.1e-183;
 Matches 540; Conservative 0; Mismatches 11; Indels 11; Gaps 4;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Db 1 MLAVGCALLAALLAALAPRCPCPAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Qy 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGVSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 61 VLKPAAGSHPSRWAGMGRLLRSVLQHDGSGVSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Qy 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKESCOLA 179
 Db 121 CFRKSPLSNVVCEWGPSTPSLTATTKAVLLVRKFQNSPAEDFQEPQYQSQKESCOLA 179
 Qy 180 VPBGDSSFFIVSMCVASSVSGSKFTQTQFGCGIQQPDPANITVAVARNPRLSVTWQ 239

Db 180 VPEGDSFFIVSMCVASSVSGSK-SKTQTFQCGIILQDPPANITVTAVARNPRLSVTWQ 238
 QY 240 DPHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWGLRHVQLRAQEF 299
 Db 239 DPHSNSSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWGLRHVQLRAQEF 298
 QY 300 QGEWSEWPEAMGTPTWTSRSPPAENESTVPMQALTTNKDDNIFRDSANATSLPVE-- 357
 Db 299 QGEWSEWPEAMGTPTWTSRSPPAENESTVPMQALTTNKDDNIFRDSANATSLPVE-- 358
 QY 358 -----FGAGLVGQFMPVPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 411
 Db 359 RGSCLGGGGGGGSLPVPVPGEDSKDVAAPHRQPLTSSERTDQIRYILDGIALRKE 418
 QY 412 TCNKNMCESSKEALAEANNLNPMAEKDGCFCGPFNEETCLVKIITGLLEFEVYLEYLO 471
 Db 419 TCNKNMCESSKEALAEANNLNPMAEKDGCFCGPFNEETCLVKIITGLLEFEVYLEYLO 478
 QY 472 NRFESSEQARAVQSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMT 531
 Db 479 NRFESSEQARAVQSTKVLIQFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMT 538
 QY 532 THILRSFKFQSSLRALRQM 553
 Db 539 THILRSFKFQSSLRALRQM 560

RESULT 3

AAW36846
 ID AAW36846 standard; protein; 525 AA.

XX AC AAW36846;

XX DT 25-MAR-2003 (revised)

XX DT 25-MAR-1998 (first entry)

XX DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.

XX KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide /label= signal_peptide

FT Protein 20..524

FT FT /note= "H-IL-6 fusion polypeptide"

FT Region 324..341

FT /label= linker region

FT /note= "Links together COOH-terminus of sIL-6R with the

FT NH2-terminus of IL-6"

XX PN WO9732891-A2.

XX PD 12-SEP-1997.

XX PF 07-MAR-1997; 97WO-DE000458.

XX PR 07-MAR-1996; 96DE-01008813.

XX PA (ANGE-) ANGEWANDTE GENTECNOLOGIE SYSTEME GMBH.

XX PI Rosejohn S;

XX DR WPI: 1997-470536/43.

XX DR N-PSDB; AAT97848.

XX PT Conjugate of two peptide(s) with mutual affinity connected by a linker -
 PT used to modulate interactions between proteins, e.g. for ex vivo
 PT expansion of human stem cells.

XX PS Disclosure; Fig 1; 19pp; German.
 XX CC This sequence represents the fusion polypeptide H-IL-6 which contains an
 CC 18 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX SQ Sequence 525 AA;

Query Match 91.4%; Score 2661; DB 2; Length 525;
 Best Local Similarity 92.4%; Pred. No. 1.2e-174;
 Matches 511; Conservative 1; Mismatches 13; Indels 28; Gaps 1;

QY 1 MLAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
 Db 1 MLAVGCCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
 QY 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNYSYVAGRPAGTVHLLVDVPPPEPOL 120
 Db 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNYSYVAGRPAGTVHLLVDVPPPEPOL 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQYSGESQKFSQCLAV 180
 Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQYSGESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIILQDPPANITVTAVARNPRLSVTWQD 240
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGIILQDPPANITVTAVARNPRLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWGLRHVQLRAQEF 300
 Db 241 PHSWNSFYRLRFELRYRAERSKFTTMMVKDLQHCVIHDAWGLRHVQLRAQEF 300
 QY 301 GEWSEWPEAMGTPTWTSRSPPAENESTVPMQALTTNKDDNIFRDSANATSLPVEFGA 360
 Db 301 GEWSEWPEAMGTPTWTSRSPPAENESTVPMQALTTNKDDNIFRDSANATSLPVEFGA 360
 QY 361 GLVLGGQFMPVPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 420
 Db 333 GSGGGSVPEVPVPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 392
 QY 421 SSKEALAEANNLNPMAEKDGCFCGPFNEETCLVKIITGLLEFEVYLEYLNRFSSSEBQ 480
 Db 393 SSKEALAEANNLNPMAEKDGCFCGPFNEETCLVKIITGLLEFEVYLEYLNRFSSSEBQ 452
 QY 481 ARVQMSKVLIOFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILRSFK 540
 Db 453 ARVQMSKVLIOFLOKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHILRSFK 512
 QY 541 EFLQSSLRALRQM 553
 Db 513 EFLQSSLRALRQM 525

RESULT 4

AAAB15404

ID AAAB15404 standard; protein; 515 AA.

XX AC AAAB15404;

XX DT 17-JAN-2001 (first entry)

XX DE IL-6R/IL-6 fusion protein.

XX KW Fusion protein; human; interleukin 6 receptor; Pichia pastoris; yeast;
 KW drug; myeloid stem cell; platelet; blood.

XX OS Homo sapiens.
 OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 57 /note= "encoded by GGC"
 XX FT Misc-difference 281 /note= "encoded by CAA"
 XX FT
 XX PN JP2000166539-A.
 XX PD 20-JUN-2000.
 XX PF 03-DEC-1998; 98JP-00343933.
 XX PR 03-DEC-1998; 98JP-00343933.
 XX PA (TOYJ) TOSOH CORP.
 XX DR WPI; 2000-485548/43.
 XX DR N-PSDB; AAA70763.
 XX
 PT Yeast of Pichia Pastoris genus transformed by expression vector
 PT containing gene encoding fused protein of interleukin-6 receptor (IL-6R)
 PT protein for amplifying myeloid stem cells and increasing platelets.
 XX PS
 XX Example 1; Page 8-10; 11pp; Japanese.
 XX CC The invention relates to the production of a fusion protein comprising
 CC the human interleukin 6 receptor (IL-6R) fused to the human IL-6 protein
 CC in a Pichia pastoris yeast cell. This sequence represents the IL-6R/IL-6
 CC fusion protein. The coding sequence for this protein is cloned into an
 CC expression vector for introduction into P. pastoris. The IL-6R protein is
 CC used as a drug for amplifying myeloid stem cells and increasing platelets
 CC in blood
 XX SQ Sequence 515 AA;
 Query Match 91.3%; Score 2658.5; DB 3; Length 515;
 Best Local Similarity 95.3%; Pred. No. 1.8e-174;
 Matches 509; Conservative 1; Mismatches 5; Indels 19; Gaps 2;
 Qy 20 LAPRCRPAQEVARGVLTSLPGDSVTLTCTCGVEPDNATVHVLKPAAGSHPSRWAGMR 79
 Db 1 LAPRCRPAQEVARGVLTSLPGDSVTLTCTCGVEPDNATVHVLKPAAGSHPSRWAGMR 60
 Qy 80 RLLRSVOLHDSGNSYCYRAGRAGTGHLLVDVPEEPOLSCFRKSPLSNVVCEWGPST 139
 Db 61 RLLRSVOLHDSGNSYCYRAGRAGTGHLLVDVPEEPOLSCFRKSPLSNVVCEWGPST 120
 Qy 140 PSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQQLAVPEGDSFYSVCMCVASSVG 199
 Db 121 PSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQQLAVPEGDSFYSVCMCVASSVG 180
 Qy 200 SKFSKTQTFQCGILQDPPNITVAVARNPRVLSVTWDPHNSNSFVRLRPELYRA 259
 Db 181 SKFSKTQTFQCGILQDPPNITVAVARNPRVLSVTWDPHNSNSFVRLRPELYRA 240
 Qy 260 ERSTFTTMMVKDLQHHCVIHDAMSLRHVVQLRAQEEFGGSEWSPEAMGTPWTESR 319
 Db 241 ERSTFTTMMVKDLQHHCVIHDAMSLRHVVQLRAQEEFGGSEWSPEAMGTPWTESR 300
 Qy 320 SPAAENEVSTPMQALTNKDDNILFRDSANATSLPVEFGAGLVLGQGFMPVPEGDSKD 379
 Db 301 SPAAENEVSTPMQALTNKDDNILFRDSANATSLPVEFGAGLVLGQGFMPVPEGDSKD 341
 Qy 380 VAAHPRQLTSSEIRIDQIRYILGIGALRKETCKNSKNCSSKEALAEANNLNPQVAK 439
 Db 342 VAAHPRQLTSSEIRIDQIRYILGIGALRKETCKNSKNCSSKEALAEANNLNPQVAK 401
 Qy 440 DGCFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVQSTKVLQFLOKKA 499

Db 402 DGCFSQGFNEETCLVKIITGLLEFEVYLYLQNRFSSEEQARAVQSTKVLQFLOKKA 461
 Qy 500 KNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLILRSKFELQSSLRALRQM 553
 Db 462 KNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLILRSKFELQSSLRALRQM 515
 RESULT 5
 AAW36847
 ID AAW36847 standard; protein; 500 AA.
 XX AC AAW36847;
 XX DT 25-MAR-2003 (revised)
 XX DT 25-MAR-1998 (first entry)
 XX DE Human fusion polypeptide H-IL-6 with 13 amino acid linker.
 XX KW Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 XX KW protein interaction; therapeutic; antagonist.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..19 /label= signal_peptide
 XX FT Protein 20..500 /note= "H-IL-6 fusion polypeptide"
 XX FT Region 304..316 /label= linker region
 XX FT /note= "links together COOH-terminus of sIL-6R with the
 XX FT NH2-terminus of IL-6"
 XX PN WO9732891-A2.
 XX PD 12-SEP-1997.
 XX PF 07-MAR-1997; 97WO-DE000458.
 XX PR 07-MAR-1996; 96DE-01008813.
 XX PA (ANGE-) ANGEWANDTE GENTECNOLOGIE SYSTEME GMBH.
 XX PI RoseJohn S;
 XX DR WPI; 1997-470536/43.
 XX DR N-PSDB; AAT97849.
 XX PT Conjugate of two peptide(s) with mutual affinity connected by a linker -
 XX PT used to modulate interactions between proteins, e.g. for ex vivo
 XX PT expansion of human stem cells.
 XX PS Disclosure; Fig 2; 19pp; German.
 XX CC This sequence represents the fusion polypeptide H-IL-6 which contains an
 CC 13 amino acid linker which joins the carboxy terminus of human
 CC interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 CC vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-
 XX CC MAR-2003 to correct PI field.)
 XX SQ Sequence 500 AA;
 Query Match 86.8%; Score 2527.5; DB 2; Length 500;
 Best Local Similarity 88.8%; Pred. No. 1.8e-165;
 Matches 491; Conservative 0; Mismatches 9; Indels 53; Gaps 2;
 Qy 1 MLAVGCALLAALAAFGAALAPRCRPAQEVARGVLTSLPGDSVTLTCTCGVEPDNATVHM 60


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Db 1 MLAVGALLAAALAAAPGAAAPRRCPAQEVARGVLTSLFGDSVTLTCFGEVEDNATVHM 60
QY 61 VLURKPAAGSHPSRWAGMRLLRLRSVOLHDSGNYSYRAGRAGVTHLLVDVPPPEQLS 120
Db 61 VLURKPAAGSHPSRWAGMRLLRLRSVOLHDSGNYSYRAGRAGVTHLLVDVPPPEQLS 120
QY 121 CFRKPSLNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQQLAV 180
Db 121 CFRKPSLNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQQLAV 180
QY 181 PEGDSSFIVSMCVASSVSGSKFTQTTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
Db 181 PEGDSSFIVSMCVASSVSGSKFTQTTFQCGILQDPDPANITVTAVARNPRLSVTWOD 240
QY 241 PHSWNSFFRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVOLRAOEFGQ 300
Db 241 PHSWNSFFRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVOLRAOEFGQ 300
QY 301 GEWSSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGA 360
Db 281 GEWSSEWSPAMGTPWTESRPPARG-----GG 307
QY 361 GLVLGGQFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCE 420
Db 308 GSGGGGSEVPPPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKNMCE 367
QY 421 SKKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVYVLELQNRPESSBEQ 480
Db 368 SKKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVYVLELQNRPESSBEQ 427
QY 481 ARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQAOQWLOQDMTTHLIRSFK 540
Db 428 ARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQAOQWLOQDMTTHLIRSFK 487
QY 541 EFLQSSLRALQM 553
Db 488 EFLQSSLRALQM 500

RESULT 6
AAAY30938
ID AAAY30938 standard; protein; 419 AA.
XX AC AAAY30938;
XX DT 19-OCT-1999 (first entry)
XX DE Human IL-6 receptor/IL-6 fusion protein.
KW IL-6; interleukin-6; receptor; human; fusion protein; bone marrow;
KW stem cell; platelet; reduced antigenicity.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Protein i..420
XX FT /note= "No start codon given"
XX PN JP11196867-A.
XX PD 27-JUL-1999.
XX PF 09-JAN-1998; 98JP-00002921.
XX PR 09-JAN-1998; 98JP-00002921.
XX PA (TOXJ) TOSOH CORP.
XX DR WPI; 1999-496648/42.
XX DR N-PSDB; AA209202.
XX

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PT New interleukin-6 receptor-interleukin-6 fused protein and gene - used
PT for growth of bone marrow stem cells and platelets.
XX
PS Example 1; Page 5-8; 8pp; Japanese.
XX
CC This invention describes a novel gene which encodes a fusion protein of
CC interleukin-6 (IL-6) receptor and bound with a gene sequence encoding for
CC IL-6 at the downstream of IL-6 receptor gene. The gene and its encoding
CC protein has applications for the growth of bone marrow stem cells and
CC platelets. Transmission of a signal of IL-6 to target cells for
CC stimulation with reduced antigenicity is possible. This sequence
CC represents the IL-6 receptor/IL-6 fusion protein described in the
CC invention
XX
SQ Sequence 419 AA;

Query Matcha 73.6%; Score 2144.5; DB 2; Length 419;
Best Local Similarity 94.1%; Pred. No. 3.5e-139;
Matches 412; Conservative 3; Mismatches 4; Indels 19; Gaps 2;

QY 116 EPQLSCFRKPSLNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFS 175
Db 1 EPQLSCFRKPSLNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFS 60
QY 176 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTTFQCGILQDPDPANITVTAVARNPRLS 235
Db 61 COLAVPEGDSSFYIVSMCVASSVSGSKFTQTTFQCGILQDPDPANITVTAVARNPRLS 120
QY 236 VTWODPHSWNSFFRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVOLRAQ 295
Db 121 VTWODPHSWNSFFRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWSGLRHVVOLRAQ 180
QY 296 EEFQGGSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLP 355
Db 181 EEFQGGSEWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNIL----- 229
QY 356 VEFQAGLVGGQFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNK 415
Db 230 ---SSELV-----APVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNK 281
QY 416 SNMCESKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVYLVYVLELQNRPE 475
Db 282 SNMCESKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLDSEVYLVYVLELQNRPE 341
QY 476 SSEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQAOQWLOQDMTTHLI 535
Db 342 SSEQARAVOMSTKVLIOFLQKAKNLDALTTPDPTTNASLLTKLQAOQWLOQDMTTHLI 401
QY 536 LRSFKFELQSSLRALQM 553
Db 402 LRSFKDFLQSSLRALQM 419

RESULT 7
AAAY2195
ID AAAY2195 standard; protein; 690 AA.
XX AC AAAY2195;
XX DT 01-AUG-2000 (first entry)
XX DE Human IL-6R-alpha-C-gamma-1 fusion protein.
XX KW IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
XX fusion protein; cytostatic; immunomodulator; osteopathic.
XX OS Synthetic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Protein 1..358
XX FT /label= IL-6R-alpha
XX FT Peptide 359..360

```

FT Protein /note= "Ala-Gly bridge"
 FT 361. .690
 FT /label= C-gamma-4

PN WO200018932-A2.
 XX 06-APR-2000.
 PD 22-SEP-1999; 99WO-US022045.
 XX 25-SEP-1998; 98US-0101858P.
 PR 19-MAY-1999; 99US-00313942.
 XX (REG-) REGENERON PHARM INC.
 PA Stahl N, Yancopoulos GD;
 PI WPI; 2000-293165/25.
 DR Isolated nucleic acid molecule for treating cytokine-related diseases or
 XX disorders encodes a fusion polypeptide capable of binding a cytokine to
 PT form a nonfunctional complex.
 PT Example 4; Page; 152pp; English.
 PS The invention concerns production of antagonists to any cytokine that
 XX utilizes an alpha specificity determining component, which when combined
 CC with the cytokine, binds to a first beta signal transducing component to
 CC form a non-functional intermediate which then binds to a second beta
 CC signal transducing component causing beta-receptor dimerization, the
 CC soluble alpha specificity determining component of the receptor (sk-
 CC alpha) and the extracellular domain of the first beta signal transducing
 CC component of the cytokine receptor (beta-1) are combined to form
 CC heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by
 CC binding the cytokine to form a non-functional complex. The receptor
 CC components are shared by cytokines such as the CNF (ciliary neurotrophic
 CC factor) family of cytokines. The invention provides the basis for the
 CC development of IL-6 antagonists, as they show that if, in the presence of
 CC a ligand, a non-functional intermediate complex, consisting of the
 CC ligand, its alpha receptor and its beta-1 receptor component, can be
 CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia

XX SQ Sequence 690 AA;

Query Match 66 24; Score 1929; DB 3; Length 690;
 Best Local Similarity 69.14; Pred. No. 4.7e-124;
 Matches 386; Conservative 29; Mismatches 66; Indels 78; Gaps 7;

Qy 1 MLAVGCAALLAALPAAGAAAPRCQAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Db 1 MVAVGCAALLAALPAAGAAAPRCQAQVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGGRLLLSVQLHDSGNYCYRAGRPAGTVHLLVDVPEEPQLS 120
 Db 61 VLKPAAGSHPSRWAGGRLLLSVQLHDSGNYCYRAGRPAGTVHLLVDVPEEPQLS 120

Qy 121 CFRKSPLSNVVCEGPRSTPLTAKVLLVRKFNQSPAEQFOEPCYQSQSKFSCOLAV 180
 Db 121 CFRKSPLSNVVCEGPRSTPLTAKVLLVRKFNQSPAEQFOEPCYQSQSKFSCOLAV 180

Qy 181 PEGDSSFFIVSMCVASSVSGSKFSKTQTFQGGIILQPDPPANITVTAVRPNRLSVTWDQ 240
 Db 181 PEGDSSFFIVSMCVASSVSGSKFSKTQTFQGGIILQPDPPANITVTAVRPNRLSVTWDQ 240

4

Qy 241 PHSWNSFYRLRPELRYRAERSKTFTTWMVKDLQHCVCVHDAWSGLRHVVQLRAQEBFGQ 300
 Db 241 PHSWNSFYRLRPELRYRAERSKTFTTWMVKDLQHCVCVHDAWSGLRHVVQLRAQEBFGQ 300

Qy 301 GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFGA 360
 Db 301 GEWSEWSPEAMGTPWTESRSPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVEFGA 360

Qy 361 GLVLGGQFMVPPGEGDS-----KD-----VAAPHRQPLT----- 389
 Db 361 ASTKGPSVFPFLAPSSKSTSGTAALGCLVKDYFPEPTVSMNSGALTSGVHTTFAVLQSS 420

Qy 390 -----SSERIDKQIRYILDGIALRKETCNKSNWCE 420
 Db 421 GLXSLSSVVTVPSSSLGTQTYICNVNHPKSNTKVDKKV-----EPKSCDKTHTCP 470

Qy 421 --SSKALAEENLNLPMKAEKDGCFQSGFNEETCLVKIIT--GLLFEFVVVLELQ--N 472
 Db 471 PCFAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 530

Qy 473 RFESSEEQARAVQMSTKVL 491
 Db 531 KTKPREEQYNSTYRVVSVL 549

RESULT 8
 AAW70797
 ID AAW70797 standard; protein; 592 AA.
 XX AAW70797;
 AC AAW70797;
 DT 03-FEB-1999 (first entry)
 XX Human interleukin-6R-alpha-Fc.
 DE gp130; cytokine antagonist; interleukin; gamma-interferon;
 KW granulocyte macrophage colony-stimulating factor; J peptide;
 KW transforming growth factor-beta.
 XX Synthetic.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Protein 1. .358
 FT /note= "human IL-R-alpha"
 FT Peptide 1. .19
 FT /note= "signal peptide"
 FT Misc-difference 2
 FT /label= L2V
 FT /note= "changed to accommodate a Kozak sequence"
 FT Misc-difference 359. .360
 FT /note= "Ala-Gly bridge"
 FT Protein 361. .592
 FT /note= "Fc domain of human IgG1"
 FT Disulfide-bond 371. .374
 XX US5844099-A.
 PN 01-DEC-1998.
 PD 27-NOV-1995; 95US-00563105.
 PF 20-OCT-1993; 93US-00140222.
 PR (REG-) REGENERON PHARM INC.
 PA Yancopoulos GD, Stahl N, Economides A;
 PI WPI; 1999-044669/04.
 DR Cytokine antagonists - comprising extracellular domains of specificity-
 XX determining and signal-transducing components of cytokine receptor.
 PT

Example 3; Fig 5; 46pp; English.

The present sequence represents the amino acid sequence of human interleukin (IL)-6R-alpha-Fc. The protein is used in the course of the invention. The specification describes cytokine antagonists comprising only the extracellular domain of the specificity-determining component of the cytokine receptor and the extracellular domain of a signal-transducing component of the cytokine receptor. The cytokine is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15), granulocyte macrophage colony-stimulating factor (GM-CSF), gamma-interferon or transforming growth factor-beta (TGF-beta). The antagonist is capable of binding the cytokine to form a nonfunctional complex. The compounds have therapeutic activity as cytokine antagonists and can also be used in assays for identifying novel agonists and antagonists of cytokines

Sequence 592 AA;

Query Match 66.2%; Score 1927.5; DB 2; Length 592;
 Best Local Similarity 72.8%; Pred. No. 4.9e-124;
 Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;
 QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHW 60
 DB 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNSCYRAGRPAGTVHLLVDVPEEPQLS 120
 QY 121 CFRKSPNSLVNVCWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESKFSQCLAV 180
 DB 121 CFRKSPNSLVNVCWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVAVARNPRLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVGSFKSTQTFQGGIILQDPPANITVAVARNPRLSVTWQD 240
 QY 241 PHSWNSSFYRLRFLRYRAERSKFTTWMVKDQHHCVIHDWGLRHVVQLRAQERFQ 300
 DB 241 PHSWNSSFYRLRFLRYRAERSKFTTWMVKDQHHCVIHDWGLRHVVQLRAQERFQ 300
 QY 301 GEWSEWSPFAMGTPWTESSRPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVERG- 359
 DB 301 GEWSEWSPFAMGTPWTESSRPPAENEVSTPMQALTTNKDDNLLFRDSANATSLPVDAG 360
 QY 360 -----AGLVLGQ-----PMVPPGSDSKDAAPHRQPL-----TSSE 393
 DB 361 BPKSCDKTHTCPPCPAPPELLGGPSVFLPFPKP-----KDTLMISRTPEVTCVVDVSHED 415
 QY 394 IDKQIRYILDGI-----SALRKETCNKSNWCESSKEALAEENLN-----LPK 435
 DB 416 PEVFPNFWVDGVEVHNATKPREBOYNSTYRVVSVLTVLHQDLNKGKYCKVSNKALPA 475
 QY 436 MAEKDGCQSQSFNER-----TCLVKTIITGLLEPEVYLVLEIQN 472
 DB 476 PIEKTIKAKGQPREPQVYVLTTPPSDELTKQVSLTCLVK---GYPYSDIAVEWESN 529

RESULT 9

ID AAY92185

XX AAY92185 standard; protein; 592 AA.

AC AAY92185;

DT 01-AUG-2000 (first entry)

DE Human IL-6R-alpha-Fc fusion protein.

XX IL-6R-alpha-Fc; cytokine; antagonist; CNTF; receptor; fusion protein;

KW cytostatic; immunomodulator; osteopathic.

XX Synthetic.

OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Protein 1..358
 FT Peptide /label= IL-6R-alpha
 FT Peptide 1..19
 FT Peptide /label= signal_peptide
 FT Peptide 359..360
 FT Protein /note= "Ala-Gly bridge"
 FT Protein 361..592
 FT Disulfide-bond /label= IgG1_Fc_domain
 FT Disulfide-bond 371
 FT Disulfide-bond /note= "forms inter-chain disulfide bridge that link two Fc domains"
 FT Disulfide-bond 374
 FT Disulfide-bond /note= "forms inter-chain disulfide bridge that link two Fc domains"
 XX WO200018932-A2.
 PD 06-APR-2000.
 XX 22-SEP-1999; 99WO-US022045.
 XX 25-SEP-1998; 98US-0101858P.
 PR 19-MAY-1999; 99US-00313942.
 XX (REGE-) REGENERON PHARM INC.
 XX Stahl N, Yancopoulos GD;
 FI WPI; 2000-293165/25.
 DR Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.
 PT Example 3; Fig 5; 152pp; English.

The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (SR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (SR-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (Ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia

Sequence 592 AA;
 Query Match 66.2%; Score 1927.5; DB 3; Length 592;
 Best Local Similarity 72.8%; Pred. No. 4.9e-124;
 Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;
 QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHW 60
 DB 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHW 60

```

QY 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
QY 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTFQCGILQPPPPANITVAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTFQCGILQPPPPANITVAVARNPRLSVTWQD 240
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDWAGSLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDWAGSLRHVVQLRAQEFQ 300
QY 301 GESEWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFG- 359
DB 301 GESEWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFG 360
QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHROPL-----TSER 393
DB 361 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPK-----KDTLMISRTPEVTCVVVDVSHED 415
QY 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAEENLN-----LPK 435
DB 416 PEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA 475
QY 436 MAEKDGCFSQGFNEE-----TCLVKIIITGLLEFVEVLEYLQN 472
DB 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

RESULT 10
ABW02165
ID ABW02165 standard; protein; 592 AA.
XX AC ABW02165;
XX DE Human IL-6Ralpha-Fc protein.
DT 12-FEB-2004 (first entry)
XX KW Cytokine; cytokine-related disease; immunomodulator; osteoporosis;
XX KW cancer; cachexia; arthritis; cytostatic; osteopathic; therapy; human.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Signal_peptide
FT Protein 20..592
FT Region /note= "Human mature IL-6Ralpha-Fc protein"
FT Protein 359..360
FT Protein /note= "Ala-Gly bridge"
FT Domain 361..592
FT Protein /note= "Human IgG1 Fc domain"
FT Disulfide-bond 371..374
FT Protein /note= "Inter-chain disulphide bridge"
XX PN US2003143697-A1.
XX PD 31-JUL-2003.
XX PF 28-OCT-2002; 2002US-00282162.
XX PR 22-SEP-1999; 99WO-US022045.
XX PR 22-MAR-2001; 2001US-00787835.
XX PA (STAHL/) STAHL N.
XX PA (YANC/) YANCOPOULOS G D.

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PI Stahl N, Yancopoulos GD;
XX WPI; 2003-851784/79.
XX PT New nucleic acid molecules encoding fusion polypeptides capable of
XX binding a cytokine to form a non-functional complex, useful for treating
XX cytokine-related diseases or disorders, e.g. cancer, cachexia, arthritis,
XX or osteoporosis.
XX PS Example 3; Fig 5; 300pp; English.
XX CC The present invention provides a novel fusion polypeptide capable of
XX binding a cytokine to form a nonfunctional complex. The invention is
XX useful for identifying agonists or antagonists of cytokine receptors and
XX for treating cytokine-related diseases or disorders e.g. cancer,
XX cachexia, arthritis and osteoporosis. The present sequence is human IL-
XX 6Ralpha-Fc protein
XX SQ Sequence 592 AA;

Query Match 66.2%; Score 1927.5; DB 7; Length 592;
Best Local Similarity 72.8%; Pred. No. 4.9e-124;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCALLAALAAFGAALAPRRCPAQEVARGLTSLPGDSVTLTCGVPEDNATVHW 60
DB 1 MVAVGCALLAALAAFGAALAPRRCPAQEVARGLTSLPGDSVTLTCGVPEDNATVHW 60
QY 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRRLRLSLVQLHDSGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQSKFSCQLAV 180
QY 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTFQCGILQPPPPANITVAVARNPRLSVTWQD 240
DB 181 PEGDSSFFIYVSMCVASSVSGSKFSTQTFQCGILQPPPPANITVAVARNPRLSVTWQD 240
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDWAGSLRHVVQLRAQEFQ 300
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMVKDLQHCVIHDWAGSLRHVVQLRAQEFQ 300
QY 301 GESEWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFG- 359
DB 301 GESEWSPEAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVEFG 360
QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHROPL-----TSER 393
DB 361 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPK-----KDTLMISRTPEVTCVVVDVSHED 415
QY 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAEENLN-----LPK 435
DB 416 PEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA 475
QY 436 MAEKDGCFSQGFNEE-----TCLVKIIITGLLEFVEVLEYLQN 472
DB 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

RESULT 11
AA92196
ID AA92196 standard; protein; 468 AA.
XX AC AA92196;
XX DT 01-AUG-2000 (first entry)
XX DE Human IL-6R-alpha-kappa fusion protein.
XX KW IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;
XX KW fusion protein; cytostatic; immunomodulator; osteopathic.

```

XX Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1..358 /label= IL-6R-alpha
FT Peptide 359..360 /note= "Ala-Gly bridge"
FT Protein 361..468 /label= kappa_domain
XX
XX WO200018932-A2.
FN
XX
XX 06-APR-2000.
XX
XX 22-SEP-1999; 99WO-US022045.
XX
XX 25-SEP-1998; 98US-0101858P.
PR 19-MAY-1999; 99US-00313942.
XX
XX (REGE-) REGENERON PHARM INC.
PA
XX Stahl N, Yancopoulos GD;
PI WPI; 2000-293165/25.
DR
XX
XX Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.
XX
XX Example 4; Page; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
XX
XX Sequence 468 AA;
Query Match 66.1%; Score 1923.5; DB 3; Length 468;
Best Local Similarity 95.5%; Pred. No. 6.8e-124;
Matches 360; Conservative 5; Mismatches 11; Indels 1; Gaps 1;
QY 1 MVAUCGALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60
DB 1 MVAUCGALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60
QY 61 VLKPKAAGSHPSRWAGMGRLLRLLSVQLHDSGNYSYRAGRPAGTVHLLVDVPPPEQLS 120
DB 61 VLKPKAAGSHPSRWAGMGRLLRLLSVQLHDSGNYSYRAGRPAGTVHLLVDVPPPEQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
QY 181 PEGDSSFYIYVMCVASSVSGSKFSTOTFOCGIILQPPPPANITVTAVARNRWLSVTWQD 240
DB 181 PEGDSSFYIYVMCVASSVSGSKFSTOTFOCGIILQPPPPANITVTAVARNRWLSVTWQD 240
QY 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFGQ 300
DB 241 PHSWNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFGQ 300
QY 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPV-BFG 359
DB 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDAG 360
QY 360 AGLVLGQPMVPVPGED 376
DB 361 SGTVAAPSVFIFFPSDE 377
RESULT 12
AAI92197
ID AAY92197 standard; protein; 477 AA.
XX
XX AC AAY92197;
XX
XX DT 01-AUG-2000 (first entry)
XX
XX DE Human IL-6R-alpha-j-kappa fusion protein.
XX
XX KW IL-6R-alpha-j-kappa; cytokine; antagonist; CNTF; receptor;
XX fusion protein; Cytostatic; Immunomodulator; osteopathic.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO200018932-A2.
XX
XX PD 06-APR-2000.
XX
XX PF 22-SEP-1999; 99WO-US022045.
XX
XX PR 25-SEP-1998; 98US-0101858P.
XX 19-MAY-1999; 99US-00313942.
XX
XX PA (REGE-) REGENERON PHARM INC.
XX
XX PI Stahl N, Yancopoulos GD;
XX
XX DR WPI; 2000-293165/25.
XX
XX PT Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine to form a nonfunctional complex.
XX
XX PS Example 4; Page; 152pp; English.
XX
XX The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sr-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sr-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokine to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha receptor and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gp130. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessible to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia
XX
XX Sequence 468 AA;
Query Match 66.1%; Score 1923.5; DB 3; Length 468;
Best Local Similarity 95.5%; Pred. No. 6.8e-124;
Matches 360; Conservative 5; Mismatches 11; Indels 1; Gaps 1;
QY 1 MVAUCGALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60
DB 1 MVAUCGALLAALLAAGALAPRRCPAQEVARGVLTSLPGDSVTLTCGVPEDNATVHM 60
QY 61 VLKPKAAGSHPSRWAGMGRLLRLLSVQLHDSGNYSYRAGRPAGTVHLLVDVPPPEQLS 120
DB 61 VLKPKAAGSHPSRWAGMGRLLRLLSVQLHDSGNYSYRAGRPAGTVHLLVDVPPPEQLS 120

CC formed, it will effectively block the action of the ligand. Effective
 CC antagonists of IL-6 or CNTF consist of heterodimers of the extracellular
 CC domains of the alpha specificity determining components of their
 CC receptors and the extracellular domain of gp130. The resultant
 CC heterodimers, function as high-affinity traps, rendering the cytokine
 CC inaccessible to form a signal transducing complex with the native
 CC membrane-bound forms of their receptor. The nucleic acids and
 CC polypeptides are useful for treating cytokine-related diseases or
 CC disorders such as osteoporosis and primary and secondary effects of
 CC cancer including multiple myeloma or cachexia
 XX
 XX SQ Sequence 477 AA;

Query Match 66.0%; Score 1922; DB 3; Length 477;
 Best Local Similarity 81.9%; Pred. No. 8.9e-124;
 Matches 376; Conservative 13; Mismatches 28; Indels 42; Gaps 6;
 QY 1 MLAVGCALLAALLAAGGALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Db 1 MWVGCALLAALLAAGGALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
 Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNRWLSVTWQD 240
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNRWLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDWSGLRHVVQLRAQEFQ 300
 Db 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDWSGLRHVVQLRAQEFQ 300
 QY 301 GEWSEWSPKAGTPTWESRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFG 357
 Db 301 GEWSEWSPKAGTPTWESRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFG 357
 QY 358 -FGAGLVGGQFMPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISAIRKETCNKS 416
 Db 361 TFGQTKV- - - - -EIKTVAPSVFTFPFS- - - - -DEQLK- - - - -SGTASVVCLLN 400
 QY 417 NMCSSKEALANNLPLKMA- - - - -EKDQCFQSGFNEET 451
 Db 401 NF- - - - -YPERAKVQWKVDNALQSGNSQES 425

RESULT 13
 AAP90284
 ID AAP90284 standard; protein; 468 AA.
 XX
 AC AAP90284;
 XX
 DT 25-MAR-2003 (revised)
 DT 31-MAR-1992 (first entry)
 XX
 DE Sequence of a receptor protein for human B cell stimulating factor-2
 DE (BSF2 receptor).
 XX
 KW B cell; immune disorder; therapy; diagnosis; prophylaxis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 2..22
 FT /label= hydrophobic region
 FT Region 362..386
 FT /label= hydrophobic region
 XX
 PN EP325474-A.

XX
 PD 26-JUL-1989.
 XX
 PF 20-JAN-1989; 89EP-00300536.
 XX
 PR 22-JAN-1988; 88JP-00012387.
 PR 25-JAN-1988; 88JP-00012599.
 PR 04-AUG-1988; 88JP-00194885.
 PR 14-JAN-1989; 89JP-00007461.
 XX
 PA (KISH/) KISHIMOTO T.
 XX
 PI Kishimoto T;
 XX
 DR WPI; 1989-214667/30.
 DR N-PSDB; AAN90340.
 XX
 PT Receptor protein for human B cell stimulating factor-2 - obt'd. by
 PT recombinant DNA techniques and used as diagnostic prophylactic or
 PT therapeutic agent.
 XX
 PS Claim 2; Page 19-21; 63pp; English.
 XX
 CC The cDNA in AAN90340 was derived from monocytic cell line U937. Isolated
 CC BSF2 receptor and DNA encoding it are claimed, as are (b) expression
 CC vectors; (c) host organisms; (d) antibodies; and (e) hybridomas. (Updated
 CC on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 468 AA;
 Query Match 65.8%; Score 1917; DB 1; Length 468;
 Best Local Similarity 96.8%; Pred. No. 1.9e-123;
 Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 QY 1 MLAVGCALLAALLAAGGALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 Db 1 MLAVGCALLAALLAAGGALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPACTVHLLVDVPPPEPQLS 120
 QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
 Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSQESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNRWLSVTWQD 240
 Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGILQPDPPANITVAVARNRWLSVTWQD 240
 QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDWSGLRHVVQLRAQEFQ 300
 Db 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCVHDWSGLRHVVQLRAQEFQ 300
 QY 301 GEWSEWSPKAGTPTWESRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFG 360
 Db 301 GEWSEWSPKAGTPTWESRSPPAENESTPMQALTTNKDDNILFRDSANATSLPVEFG 360
 QY 361 G- - - - -LVLGG 366
 Db 361 SVPLPTFLVAGG 372
 RESULT 14
 AAR37215
 ID AAR37215 standard; protein; 468 AA.
 XX
 AC AAR37215;
 XX
 DT 13-SEP-1993 (first entry)
 XX
 DE IL-6 receptor.
 XX

KW Interleukin-6; IL-6; receptor; immunoglobulin-like; domain; truncated;
 KW transmembrane; multiple myeloma; binding; ability; signal transfer;
 KW disease; intracellular.
 XX Synthetic.
 OS
 XX
 XX JP05091892-A.
 XX
 XX 16-APR-1993.
 PD
 XX
 XX 02-OCT-1991; 91JP-00255521.
 PF
 XX
 XX 02-OCT-1991; 91JP-00255521.
 PR
 XX
 XX (KISH/) KISHIMOTO C.
 PA (CHUS) CHUGAI PHARM CO LTD.
 PA (TOYO) TOSOH CORP.
 XX
 XX WPI; 1993-161739/20.
 DR N-PSDB; AAQ41746.
 DR
 XX
 XX New interleukin-6 receptor deriv. - for treating diseases caused by IL-6,
 PT e.g. multiple myeloma.
 PT
 XX
 XX Disclosure; Page 10-12; 23pp; Japanese.
 PS
 XX
 XX This sequence represents an interleukin-6 (IL-6) receptor. Variants of
 CC the receptor lacking either the immunoglobulin-like domain or the
 CC transmembrane and intracellular domain have IL-6 binding ability and
 CC signal transfer ability. Either the full length or truncated IL-6
 CC receptors may be used for diseases caused by IL-6 such as multiple
 CC myeloma
 CC
 XX
 XX Sequence 468 AA;

Query Match 65.8%; Score 1917; DB 2; Length 468;
 Best Local Similarity 96.8%; Pred. No. 1.9e-123;
 Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 QY 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 DB 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 QY 121 CFRKPSLNNVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSESQKFSQCLAV 180
 DB 121 CFRKPSLNNVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILOPDPANITVTAVARNRWLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILOPDPANITVTAVARNRWLSVTWQD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEFQ 300
 DB 241 PHSWNSFFYRLRFELRYAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEFQ 300
 QY 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360
 DB 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360
 QY 361 G-----LVLG 366
 DB 361 SVPLPTFLVAGG 372
 RESULT 15
 AAB36655
 ID AAB36655 standard; protein; 468 AA.
 XX
 AC AAB36655;

XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human IL-6 receptor subunit alpha protein SEQ ID NO:12.
 XX
 XX DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200073451-A1.
 PN
 XX 07-DEC-2000.
 PD
 XX
 XX 30-MAY-2000; 2000WO-US014867.
 PF
 XX
 XX 01-JUN-1999; 99US-00322913.
 PR
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX
 XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
 PI WPI; 2001-061536/07.
 XX
 XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
 PT useful for regulating immune system function and for treating
 PT immunological disorders.
 PT
 XX
 PS Disclosure; Page 13-15; 93pp; English.
 PS
 XX
 XX The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide. The
 CC DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for detecting
 CC presence of their ligands and in drug screening assays. It is also useful
 CC for treating conditions such as immunological disorders. The present
 CC sequence represents a cytokine receptor subunit protein which is given in
 CC an alignment of various cytokine receptor subunits in the exemplification
 CC of the present invention
 CC
 XX
 XX Sequence 468 AA;

Query Match 65.8%; Score 1917; DB 4; Length 468;
 Best Local Similarity 96.8%; Pred. No. 1.9e-123;
 Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 QY 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 DB 1 MLAVGALLAALLAALPAGALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
 QY 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 DB 61 VLKPAAGSHPSRWAGMGRLLRLSVQLHDSGNYSCYRAGRAGTVHLLVDVPPPEPQLS 120
 QY 121 CFRKPSLNNVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSESQKFSQCLAV 180
 DB 121 CFRKPSLNNVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQPCQYSESQKFSQCLAV 180
 QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILOPDPANITVTAVARNRWLSVTWQD 240
 DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQCGILOPDPANITVTAVARNRWLSVTWQD 240
 QY 241 PHSWNSFFYRLRFELRYAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEFQ 300
 DB 241 PHSWNSFFYRLRFELRYAERSKFTTMMVKDLQHCCHVHDAWSGLRHVVQLRAQEFQ 300
 QY 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360
 DB 301 GEWSWSPAMGTPWTESRPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFGA 360
 QY 361 G-----LVLG 366

Db 361 SVPLPTFLVAGG 372
|||

Search completed: September 7, 2006, 22:57:55
Job time : 196 secs

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OM protein - protein search, using sw model

Run on: September 7, 2006, 22:58:10 ; Search time 42 Seconds
(without alignments)
1266.854 Million cell updates/sec

Title: US-09-462-416A-13
Perfect score: 2912
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILRSFKFLOSLRALRQM 553

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1917	65.8	468	1 A41242	interleukin-6 rece
2	954	32.8	440	2 JLO144	interleukin-6 rece
3	953.5	32.7	460	2 JLO145	interleukin-6 rece
4	947.5	32.5	212	1 IVHUB2	interleukin-6 prec
5	856.5	29.4	462	1 A37986	interleukin-6 prec
6	580.5	19.9	208	2 T09216	interleukin-6 prec
7	569	19.5	212	2 I46621	prointerleukin 6 -
8	568	19.5	212	2 I46590	interleukin 6 - pi
9	480.5	16.5	208	1 A56610	interleukin-6 prec
10	478.5	16.4	207	2 I46084	interleukin 6 - ca
11	474.5	16.3	208	1 S29549	interleukin-6 - sh
12	397	13.6	211	2 A34247	interleukin-6 prec
13	376	12.9	211	1 ICM86	interleukin-6 prec
14	339.5	11.7	422	2 I37891	interleukin-11 rec
15	335	11.5	432	2 I48343	interleukin-11 rec
16	314.5	10.8	372	2 I58141	ciliary neurotroph
17	309.5	10.6	372	1 URHUCN	ciliary neurotroph
18	302.5	10.4	362	2 S60614	growth promoting a
19	226	7.8	53	2 I53394	soluble interleuki
20	198.5	6.8	328	2 A38957	interleukin 12B pr
21	180	6.2	831	2 JQ1655	prolactin receptor
22	171.5	5.9	830	2 I50455	prolactin receptor
23	171	5.9	581	2 I45971	prolactin receptor
24	170	5.8	918	2 A4257	interleukin-6 sign
25	167.5	5.8	917	2 I43699	glycoprotein 130 -
26	164.5	5.6	918	2 A36337	membrane glycoprot
27	160	5.5	616	2 A30304	prolactin receptor
28	159	5.5	310	2 A29884	prolactin receptor
29	159	5.5	412	2 A41070	prolactin receptor

ALIGNMENTS

RESULT 1

A41242
N:Contains: interleukin-6 receptor - human
C:Species: Homo sapiens (man)
C:Date: 27-Mar-1992 #sequence revision 02-Dec-1994 #text_change 09-Jul-2004
C:Accession: A41242; J00080; S17468; A61459; S14621
R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Science 241, 825-828, 1988
A:Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A:Reference number: A41242; MUID:88305347; PMID:3136546
A:Accession: A41242
A:Molecule type: mRNA
A:Residues: 1-468 <YAM>
A:Cross-references: UNIPROT:P08887; UNIPARC:UPI00000358BA; GB:M20566; NID:G33845; PIDN:R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, Proc. Jpn. Acad. 64, 209-211, 1988
A:Title: Molecular structure of interleukin 6 receptor.
A:Reference number: J00080
A:Accession: J00080
A:Molecule type: mRNA
A:Residues: 1-468 <YA2>
A:Cross-references: UNIPARC:UPI00000358BA
R:Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich, Biochem. J. 277, 659-664, 1991
A:Title: Structural and functional studies on the human hepatic interleukin-6 receptor
A:Reference number: S17468; MUID:91336983; PMID:1872801
A:Accession: S17468
A:Molecule type: mRNA
A:Residues: 1-468 <SCH>
A:Cross-references: UNIPARC:UPI00000358BA; EMBL:X58298; NID:G32580; PIDN:CAA41231.1; P:R:Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M. J. Exp. Med. 170, 1409-1414, 1989
A:Title: Soluble cytokine receptors are present in normal human urine.
A:Reference number: A61459; MUID:90010793; PMID:2529343
A:Accession: A61459
A:Molecule type: protein
A:Residues: 20-49 <NOV>
A:Cross-references: UNIPARC:UPI000002CF0B
C:Comment: Through this receptor, interleukin-6 induces proliferation, activation, and C:Genetics: This growth factor receptor does not have a tyrosine kinase domain.
A:Gene: GDB:IL6R
A:Cross-references: GDB:127966; OMIM:147880
A:Map position: 1q21-1q21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immun: C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-468/Product: interleukin-6 receptor #status predicted <MAT>
F:20-363/Domain: extracellular #status predicted <EXT>
F:40-98/Domain: immunoglobulin homology <IMM2>

lactogen receptor
prolactin receptor
interleukin 12 p40
prolactin receptor
prolactin receptor
prolactin receptor
prolactin receptor
protein-tyrosine k
Down syndrome cell
receptor tyrosine
prolactin receptor
prolactin receptor
prolactin receptor
leptin receptor, i
protein-tyrosine k
granulocyte colony

30 159 5.5 610 2 A34631
31 159 5.5 610 2 A36116
32 158.5 5.4 335 2 I72789
33 155 5.3 292 2 I77525
34 155 5.3 303 2 I77524
35 155 5.3 608 2 I53269
36 155 5.3 630 2 I51086
37 149 5.1 890 1 A53743
38 144 4.9 1896 2 T08851
39 140.5 4.8 882 2 I38912
40 138 4.7 288 2 B59405
41 138 4.7 376 2 A59405
42 138 4.7 622 2 A40144
43 133.5 4.6 895 2 S74225
44 132.5 4.6 880 1 J04166
45 131 4.5 837 2 A34898

F:121-309/Domain: cytokine receptor homology <CRS>
E:364-386/Domain: transmembrane #status predicted <TM>
F:387-468/Domain: intracellular #status predicted <INT>
F:47-96/Disulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.8%; Score 1917; DB 1; Length 468;
Best Local Similarity 96.8%; Pred. No. 1.4e-128;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRLRSVLQHDGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Db 61 VLKRPAGSHPSRWAGMGRLLRLRSVLQHDGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQG 300
Db 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQG 300

Qy 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVFEFGA 360
Db 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQDSS 360

Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372

RESULT 2
JL0144
interleukin-6 receptor precursor (clone lambda p1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0144
R:Sugita, T.; Totusaka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A:Reference number: JL0144; MUID:90278354; PMID:2112585
A:Accession: JL0144
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <SUG>
A:Cross-references: UNIPROT:P22272; UNIPARC:UPI000011F3D9; GB:X51976; NID:G53548; PIDN:C
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C:Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-440/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 32.8%; Score 954; DB 2; Length 440;
Best Local Similarity 48.0%; Pred. No. 3.6e-60;
Matches 195; Conservative 50; Mismatches 127; Indels 34; Gaps 7;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLTVGCTLLVALLAALPAVALVGLSCRALEVANGTVTSLPGATVTLICPGKEAGNVTHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRLRSVLQHDGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Db 61 VY-----SGSQNRWTTTGTNTLVLRDVLSDTGDYLCSLNDHLVGTVLLVDVPPPEPKLS 116

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLA 179
Db 117 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLA 176

Qy 180 VPEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRWLSVTWQ 239
Db 177 ILEGDKYHIVSLCVANSVSGSKSHNEAFHSLKMWQDPPANLVVSAIPGRPRWLKYSWQ 236

Qy 240 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQG 299
Db 237 HPETWDPYSYLLQPLRYRPMWSKEFTVLLLPVAQYQCVIHDALRGVKKVQVQVGRKEBLD 296

Qy 300 QGEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSL--PV 356
Db 297 LGQWSEWSPVETGPTWIAEPRTTPA-GILWNPTQVSVEDSANHEDQYESSTEATSVLAPV 355

Qy 357 EFAGAG-----LVLGQGF-----MPVPPGGDS 377
Db 356 QESSMSLPTFLVAGGSLAFGLLLCVFIILCWEPRPHSPLODGDAS 401

RESULT 3
JL0145
interleukin-6 receptor precursor (clone lambda 301) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0145; S14543
R:Sugita, T.; Totusaka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle gene
A:Reference number: JL0144; MUID:90278354; PMID:2112585
A:Accession: JL0145
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-460 <SUG>
A:Cross-references: UNIPROT:P22272; UNIPARC:UPI0000022D4B; GB:X51975; NID:G49725; PIDN:
A:Experimental source: clone lambda 301
R:Florillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A:Description: Cloning and expression of murine IL-6 receptor.
A:Reference number: S14543
A:Accession: S14543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373,'R',375-460 <FIO>
A:Cross-references: UNIPARC:UPI000016CE46; EMBL:X53802; NID:G52692; PIDN:CAA37810.1; PI
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immun
C:Keywords: cytokine receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 32.78%; Score 953.5; DB 2; Length 460;
Best Local Similarity 50.8%; Pred. No. 4.2e-60;
Matches 191; Conservative 49; Mismatches 121; Indels 15; Gaps 6;

Qy 1 MLAVGCALLAALLAALAPRCPCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLTVGCTLLVALLAALPAVALVGLSCRALEVANGTVTSLPGATVTLICPGKEAGNVTHW 60

Qy 61 VLKRPAGSHPSRWAGMGRLLRLRSVLQHDGNSCYRAGRAGTGVHLLVDVPPPEPQLS 120
Db 61 VY-----SGSQNRWTTTGTNTLVLRDVLSDTGDYLCSLNDHLVGTVLLVDVPPPEPKLS 116

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLA 179
Db 117 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEFDQPCQYSQESQKFSCOLA 176

Qy 180 VPEGDSSFYIVSMCVASSVSGSKFSTQTFQCGGILQDPDPANITVTAVARNPRWLSVTWQ 239
Db 177 ILEGDKYHIVSLCVANSVSGSKSHNEAFHSLKMWQDPPANLVVSAIPGRPRWLKYSWQ 236

Db 177 ILEGGKVYHIVSLCVANSVSGSKSSHNEAFHSLKMQVDPDPANLVVSAIFCRPRWLKVSQ 236

QY 240 DPHSNWSSFYRLRFELRYAERSKTPTTWNVKDLQHCIVHDAMSLRHVVOLRAQEEFG 299

Db 237 HETWDPSSYLLQFQRLRYPVWSKEFTVLLPVAQCIVHDALRGVKKVQVRGKEELD 296

QY 300 QGEWSWSPEAMGTPM-TESRSPPAENVESTPMQALTNKDDNNILFRDSANATSL--PV 356

Db 297 LGQWSWSPEVCTGPIAEPRTTPA-GILWNPQTQSVSDSANHDDQYESSTEATSVLAPV 355

QY 357 EFGAG-----LVGG 366

Db 356 QESSMSLPTFLVAGG 371

RESULT 4

IVHUB2

N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell interleukin-6 precursor [validated] - human on factor

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27

R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Mateuda, T.; Nakai, S.; Kishimoto

EMBO J. 6, 2939-2945, 1987

A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene

A;Reference number: A32648; MUID: 88082664; PMID: 3500852

A;Accession: A32648

A;Molecule type: DNA

A;Residues: 1-212 <YAS>

A;Cross-references: UNIPROT:P05231; UNIPARC:UPI000002C4A6; GB:X04430; NID:G29494; PIDN:C

A;Note: the authors translated the codon CAG for residue 130 as Glu

R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.

EMBO J. 5, 2529-2537, 1986

A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a disti

A;Reference number: A91051; MUID: 87053818; PMID: 3023045

A;Accession: A25692

A;Molecule type: mRNA

A;Residues: 1-212 <ZIL>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G

R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura

i, T.; Kishimoto, T.

Nature 324, 73-76, 1986

A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocy

A;Reference number: A93387; MUID: 87065033; PMID: 3491322

A;Accession: A26966

A;Molecule type: mRNA

A;Residues: 1-212 <HIR>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04602; NID:G33849; PIDN:CAA28268.1; PID:G

R;Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.

Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989

A;Title: Deletion of 3' untranslated region of human BSP-2 mRNA causes stabilization of

A;Reference number: A33515; MUID: 89391958; PMID: 2789513

A;Accession: A33515

A;Molecule type: mRNA

A;Residues: 1-212 <TON>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M29150; NID:gi86349; PIDN:AAA59154.1; PID:

R;Haegeman, G.; Content, J.; Volktaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.

Eur. J. Biochem. 159, 625-632, 1986

A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h

A;Reference number: A25801; MUID: 87004603; PMID: 3758081

A;Accession: A25801

A;Molecule type: DNA; mRNA

A;Residues: 1-212 <HAE>

A;Cross-references: UNIPARC:UPI000002C4A6; GB:X04403

A;Experimental source: fibroblast

R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986

A;Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA

A;Reference number: A25921; MUID: 87067433; PMID: 3538015

A;Accession: A25921

A;Molecule type: mRNA

A;Residues: 1-212 <MAY>

A;Cross-references: UNIPARC:UPI000017366C

A;Cross-references: UNIPARC:UPI000002C4A6; GB:M14584; NID:gi84628; PIDN:AAA52728.1; P
R;Wong, G.G.; Mitek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
Behring Inst. Mitt. 83, 40-47, 1988
A;Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
A;Reference number: I52193; MUID: 89193317; PMID: 3266463
A;Accession: I52193
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-212 <WON>
A;Cross-references: UNIPARC:UPI000002C4A6; GB:M54894; NID:gi86351; PIDN:AAC41704.1; P
R;Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
J. Immunol. 139, 4116-4121, 1987
A;Title: Molecular cloning and expression of hybridoma growth factor in Escherichia co
A;Reference number: I56003; MUID: 88088768; PMID: 3320204
A;Accession: I56003
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-212 <BRA>
A;Cross-references: UNIPARC:UPI000002C4A6; GB:M18403; NID:gi84631; PIDN:AAAS2729.1; P
R;Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
J. Immunol. 140, 1534-1541, 1988
A;Title: Separation and comparison of two monokines with lymphocyte-activating factor
A;Reference number: A92816; MUID: 88154445; PMID: 3279116
A;Accession: A27601
A;Molecule type: protein
A;Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
A;Cross-references: UNIPARC:UPI0000173666
A;Accession: B27601
A;Molecule type: protein
A;Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
A;Cross-references: UNIPARC:UPI0000173666
R;Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
J. Immunol. 144, 1808-1816, 1990
A;Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involve
A;Reference number: A60400; MUID: 90171574; PMID: 2307841
A;Accession: A60400
A;Molecule type: protein
A;Residues: 30-43 <YAM>
A;Cross-references: UNIPARC:UPI0000173668
R;Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu
Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
A;Title: Human beta-cell differentiation factor defined by an anti-peptide antibody an
A;Reference number: A29085; MUID: 87092370; PMID: 3491991
A;Accession: A29085
A;Molecule type: protein
A;Residues: 29-42 <HIR2>
A;Cross-references: UNIPARC:UPI0000173669
R;Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.;
Anticancer Res. 11, 961-968, 1991
A;Title: Purification and characterization of human fibroblast derived differentiation
A;Reference number: A61159; MUID: 91290785; PMID: 1648338
A;Accession: A61159
A;Molecule type: protein
A;Residues: 30-42 <NOD>
A;Cross-references: UNIPARC:UPI000017366A
A;Experimental source: fibroblast
R;Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
J. Mol. Cell. Immunol. 4, 203-212, 1989
A;Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor
A;Reference number: A61462; MUID: 90121567; PMID: 2610854
A;Accession: A61462
A;Molecule type: protein
A;Residues: 28-48 <MIN>
A;Cross-references: UNIPARC:UPI000017366B
A;Experimental source: leukocyte-conditioned medium
R;May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
Cytokine 3, 204-211, 1991
A;Title: Marked cell-type-specific differences in glycosylation of human interleukin-6
A;Reference number: A48419; MUID: 91355644; PMID: 1883960
A;Accession: A48419
A;Molecule type: protein
A;Residues: 30-37, 'X', 39-40 <MAY2>
A;Cross-references: UNIPARC:UPI000017366C

A;Experimental source: FS-4 fibroblasts
A;Note: sequence extracted from NCBI backbone
A;Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form c
A;Accession: C48419
A;Molecule type: protein
A;Residues: 28-40 <MAY3>
A;Cross-references: UNIPARC:UPI00000353C4
A;Experimental source: FS-4 fibroblasts
A;Note: sequence extracted from NCBI backbone (NCBIP:63787)
A;Note: this 23-25K form contained O-linked but not N-linked carbohydrate
R;Orita, T.; Obeda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
J. Biochem. 115, 345-350, 1994
A;Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produ
A;Reference number: JX0305; MUID:94266765; PMID:8206884
R;Clouston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
Arch. Biochem. Biophys. 272, 144-151, 1989
A;Title: Disulfide structures of human interleukin-6 are similar to those of human granu
A;Reference number: S04981; MUID:89286115; PMID:2472117
A;Contents: annotation; disulfide bonds in recombinant protein
R;Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
Biochemistry 33, 5146-5154, 1994
A;Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
A;Reference number: A54253; MUID:94227044; PMID:8172889
C;Contents: annotation; lability and functional significance of each disulfide bond
C;Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factor
lobulin secretion). It therefore appears to function as an autoregulator of cell growth
C;Comment: This protein plays a regulatory role in various host defense mechanisms and e
C;Genetics:
A;Gene: GDB:IL6
A;Cross-references: GDB:120748; OMIM:147620
A;Map position: 7p21-7p21
A;Introns: 7/1; 70/3; 108/3; 157/3
C;Superfamily: interleukin-6
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-212/Product: interleukin-6, long form #status experimental <MAYL>
F;30-212/Product: interleukin-6, short form #status experimental
F;72-78,101-111/Disulfide bonds: #status experimental
F;73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;172/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 32.5%; Score 947.5; DB 1; Length 212;
Best Local Similarity 95.0%; Pred. No. 3.9e-60;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
Qy 355 PVFEGAG--LVLGQF-MPVPPGDSKDVAAPHROPLTSSBRIDKQIRYILDGISALRKE 411
Db 11 PVAFSLGLLLVLPAPFAPVPFGDSKDVAAPHROPLTSSBRIDKQIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAEANNLKPMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNKSNNCESSKEALAEANNLKPMAEKDGCQFSGFNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRPESSEQARAVQSTKVLQIFLQKAKNLDAITTPDPTNASLLTKLQANQWLQDMT 531
Db 131 NRPESSEQARAVQSTKVLQIFLQKAKNLDAITTPDPTNASLLTKLQANQWLQDMT 190
Qy 532 THLILRSFKFLQSSLRALQM 553
Db 191 THLILRSFKFLQSSLRALQM 212
RESULT 5
A37986
interleukin-6 precursor - rat
N;Alternate names: IL-6 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A37986
R;Baumann, M.; Baumann, H.; Fey, G.H.
J. Biol. Chem. 265, 19853-19862, 1990

A;Title: Molecular cloning, characterization and functional expression of the rat liver
A;Reference number: A37986; MUID:91060602; PMID:2174054
A;Accession: A37986
A;Molecule type: mRNA
A;Residues: 1-462 <BAU>
A;Cross-references: UNIPROT:P22273; UNIPARC:UPI0000167A93; GB:M58587; GB:J05668; NID:92
C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is e
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor; transmembrane protein
C;Keywords: acute phase; cytokine receptor; cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-462/Product: interleukin-6 receptor #status predicted <NAT>
F;20-362/Domain: extracellular #status predicted <EXT>
F;40-94/Domain: immunoglobulin homology <IMW>
F;117-306/Domain: cytokine receptor homology <CRS>
F;363-385/Domain: transmembrane #status predicted <TMM>
F;386-462/Domain: intracellular #status predicted <INT>
F;47-92/Disulfide bonds: #status predicted
Query Match 29.4%; Score 856.5; DB 1; Length 462;
Best Local Similarity 47.5%; Pred. No. 3.3e-53;
Matches 182; Conservative 49; Mismatches 123; Indels 29; Gaps 7;
Qy 1 MLAVGCALLAALLAALPAQAALAPRRCPAQEVARGLVLTSLPGDSVTLTCLPGVEPEDNATVHW 60
Db 1 MLAGVCTLLVALLAARPAVALVLSGRALVANGTVTSLPGATVTLICPGKEAAGNATIHW 60
Qy 61 VLKRPAGSHPSRWAGRBLRLRSVOLHDSGNVSVYRAGRAGTAVHLLVDVPPPEPQLS 120
Db 61 VY----SGSQSREWTTTNGTLLVLRVQVNDTHYLCFLDDHDLVGTPLLVDPVPEEPKLS 116
Qy 121 CFRKSPLSNVVCEWGRSTSLTKAVLLVRKQNSPAE-DFQEPCCOYSQESQKFSCOLA 179
Db 117 CFRKNPLVNAFCBWHPSSTPSTTKAVMFAKKINTNGKSDFPQPCOYSQOLKSFSCVE 176
Qy 180 VPBGDSDFYIVSMCVASSVSGSKFSKTQTFQCGILQDPPANITVTAVARN-----PR 232
Db 177 ILEGDKYHIVSLCVANSVSGSRSHNVVFSQSLXWQDPPANLVVSAIPGSLVSGSKSVGK 236
Qy 233 WLSVTWQDPHSMNSFVRLRFLRYRAERSKTTTMMVKDLQHHCHVTHDWSGLRHVVQL 292
Db 237 TLPSPGTQVTTCCNSSFTDLYGQR-----TFTWPLQVAQHQCQVTHDALRGVKKVVQV 289
Qy 293 RAQEEFGQGEWSPEAMCTPW-TESRPPAEVNEVTPMQALTNNKDDDDNILPRDSANA 351
Db 290 RGKEEDIGQWSKWSPEVTGTPLAEPRITPA-GIPGNPTQVSVEDYDNHEDQYGSSTEA 348
Qy 352 TSL-----PVEFGAGLVLG 366
Db 349 TSVLAPVQGSPIPLPTFLVAGG 371
RESULT 6
T09216
interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09216
R;Swiderski, C.E.; Horohov, D.W.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z16613
A;Accession: T09216
A;Status: preliminary; translated from GB/EMBL/DBDJB
A;Molecule type: mRNA
A;Residues: 1-208 <SWI>
A;Cross-references: UNIPROT:Q95181; UNIPARC:UPI000016C42F; EMBL:U64794; NID:92654387; I
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor
Query Match 19.9%; Score 580.5; DB 2; Length 208;
Best Local Similarity 57.3%; Pred. No. 4.7e-34;
Matches 118; Conservative 33; Mismatches 48; Indels 7; Gaps 4;

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QY 351 ATSLPVEFGAG--LVLGQGF-MPVPPGDSKDVAAAPHRQPLTSSRIDKQIRYILDGISA 407
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 7 STVTPVAFSLGILLVMATAFPTPLGEDTTSNGP---LLTADKTKQHIKYILGKISA 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 408 LRKETCNKNMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYL 467
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 LKNECNNSKCEKSEKVEALAENNLNLPKMAEKDGCFCQSGFNEETCLMKITTTGLSFBFIYL 123
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 468 EYLQNRFSSEBEQARAVQMSKVLIOFLQKAKNLDIAITTPDPTTNASLLTKLOAQNW 527
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 EYLQNEFKGEKENIKTMQISTKVLQVILMOKMKNPE-VTTTPDTAKSLLAKLHQNWL 182
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 528 QDMTTHILRSFKFQSSLRALQM 553
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 KNTTTHILRSLEDFLQFSRAIRIM 208
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
I46621
p:interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46621
R:Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
A:Reference number: I46621; MUID:91338547; PMID:1873476
A:Accession: I46621
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <RIC>
A:Cross-references: UNIPROT:P26893; UNIPARC:UPI000015C6B9; GB:M86722; NID:g164624; PIDN:
C:Genetics:
A:Gene: IL6
C:Superfamily: interleukin-6

Query Match 19.5%; Score 569; DB 2; Length 212;
Best Local Similarity 56.5%; Pred. No. 3.2e-33;
Matches 118; Conservative 33; Mismatches 54; Indels 4; Gaps 2;

QY 348 SANATSLPVEFGAGLVGQGFMPVPPG---EDSKVAAPHRQPLTSSRIDKQIRYILDG 404
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 STSAFS-PVAFSLGILLVMATAFPTPGRLGEDAKGATSDKMLFTSPDKTEELIKYILGK 63
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 405 ISALRKETCNKNMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFE 464
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 ISAMRKEMCEKCEKSEKVEALAENNLNLPKMAEKDGCFCQSGFNEETCLMRITTTGLVFEQ 123
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 465 VYLEYLQNRFSSEBEQARAVQMSKVLIOFLQKAKNLDIAITTPDPTTNASLLTKLOAQN 524
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 IYLDVLOKYEYENKGNVEAVQISTKALIQTLRQKGNPKATTPPTTNAGLLDKLQSQN 183
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 525 QWLQDMTTHILRSFKFQSSLRALQM 553
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 EWMKNTKIILRSLEDFLQFSRAIRIM 212
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
I46590
interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conce
A:Reference number: I46590; MUID:92360284; PMID:1497880
A:Accession: I46590
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <MAT>
A:Cross-references: UNIPROT:P26893; UNIPARC:UPI000012D4E5; GB:M80258; NID:g164514; PIDN:
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C:Genetics:
A:Gene: IL-6
C:Superfamily: interleukin-6

Query Match 19.5%; Score 568; DB 2; Length 212;

Best Local Similarity 56.5%; Pred. No. 3.7e-33;

Matches 118; Conservative 33; Mismatches 54; Indels 4; Gaps 3;

QY 348 SANATSLPVEFGAGLVL-GGQFMPVPP--GEDSKVAAPHRQPLTSSRIDKQIRYILDG 404

Db 5 STSAFS-PVAFSLGILLVMATAFPTPERLEEDAKGATSDKMLFTSPDKTEELIKYILGK 63

QY 405 ISALRKETCNKNMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFE 464

Db 64 ISAMRKEMCEKCEKSEKVEALAENNLNLPKMAEKDGCFCQSGFNEETCLMRITTTGLVFEQ 123

QY 465 VYLEYLQNRFSSEBEQARAVQMSKVLIOFLQKAKNLDIAITTPDPTTNASLLTKLOAQN 524

Db 124 IYLDVLOKYEYENKGNVEAVQISTKALIQTLRQKGNPKATTPPTTNAGLLDKLQSQN 183

QY 525 QWLQDMTTHILRSFKFQSSLRALQM 553

Db 184 EWMKNTKIILRSLEDFLQFSRAIRIM 212

RESULT 9

A56610

interleukin-6 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A56610; S22162

R:Broogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.

DNA Seq. 2, 411-413, 1992

A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.

A:Reference number: A56610; MUID:93076003; PMID:1446077

A:Accession: A56610

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-208 <DRO>

A:Cross-references: UNIPROT:P26892; UNIPARC:UPI000012D4D9; EMBL:X57317; NID:g2193; PID

A:Experimental source: BLV induced B cell-lymphosarcoma

A>Note: sequence extracted from NCBI backbone (NCBIP:118917)

C:Superfamily: interleukin-6

C:Keywords: cytokine

Query Match 16.5%; Score 480.5; DB 1; Length 208;

Best Local Similarity 49.8%; Pred. No. 6e-27; Mismatches 34; Indels 5; Gaps 3;

Matches 100; Conservative 34; Mismatches 62; Indels 5; Gaps 3;

QY 352 TSLPVEFGAGLVGQGF-MPVPPGDSKDVAAAPHRQPLTSSRIDKQIRYILDGISA 410

Db 10 TPFVAVSLGILLVMATAFPTPGPLGEDFKNDITTPGRLLLTTPKTEALIKRMVDKISAMRK 69

QY 411 ETCNKNMCESSKEALAENNLNLPKMAEKDGCFCQSGFNEETCLVKIITGLLEFEVYLEYL 470

Db 70 EICEKNDECESSKETLAENKLNLPKMEKDCGFCQSGFNOAICLIIRTTAGLLEYQIYLDYL 129

QY 471 QNRFESSEBEQARAVQMSKVLIOFLQKAKNLDIAITTPDPTTNASLLTKLOAQNW 530

Db 130 QNEYEGNQENVDLRNRTLIQIL--KQKIADLIT--PATNTDLLEKMQSSNEWVKNA 185

QY 531 TTHILRSFKFQSSLRALR 551

Db 186 KIILILRNLENFLQFSRAIR 206

RESULT 10

I46084

interleukin 6 - cat

C:Species: Felis silvestris catus (domestic cat)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004

C:Accession: I46084

R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.

Qy	355	PVEP-GAGLVLGQGF--MPVPPGEDSKDVAAPHROPLTSSERIDKQIRVILDGISALRKE 411
Db	11	PVAFPLGLMLVTTTAPFTPSQVRGDFTEP-TTPNRPVVTTSQVGGLIITHVLWEIVEMRKE 68
Qy	412	TCNKSNCSESSKEALAEANNLMPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYEYLO 471
Db	69	LCNGNSDCMNDALAEANNLKLPEIQRNDGCYQGYNQEIICLLKISSGGLLEHYHYLEYMK 128
Qy	472	NRP-ESSEQARAVQMSTKVLIQLQKAKNLDALITPDPTTNASLLTKLQAOQNQLQDM 530
Db	129	NNLKDNKKDKARVLQRTDTETLIHFNQEVKHLKIVLPTPISNALLTDKLESQKEWLRTK 188
Qy	531	TTTHLILSFKEFLQSSLRALRQ 552
Db	189	TIQILKLSBEFLKVTLRSTRQ 210
RESULT 14		
I37891		
interleukin-11 receptor alpha chain - human		
C/Species: Homo sapiens (man)		
C/Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004		
A/Accession: J37891; G01970; G01971		
R/Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; M		
Blood 86, 2534-2540, 1995		
A/Title: Molecular cloning of two isoforms of a receptor for the human hematopo		
A/Reference number: J37891; MUID:95399754; PMID:7670098		
A/Accession: J37891		
A/Status: preliminary; translated from GB/EMBL/DBJ		
A/Molecule type: mRNA		
A/Residues: 1-422 <RES>		
A/Cross-references: UNIPROT:Q16542; UNIPARC:UPI00000358B9; EMBL:Z38102; NID:99		
R/Van Leuven, F.		
submitted to the EMBL Data Library, July 1995		
A/Reference number: G08959		
A/Accession: G01970		
A/Status: preliminary; translated from GB/EMBL/DBJ		
A/Molecule type: DNA		
A/Residues: 1-422 <V>		
A/Cross-references: UNIPARC:UPI00000358B9; EMBL:U32323; NID:9975334; PIDN:AA83		
R/Van Leuven, F.		
submitted to the EMBL Data Library, July 1995		
A/Reference number: G08961		
A/Accession: G01971		
A/Status: preliminary; translated from GB/EMBL/DBJ		
A/Molecule type: mRNA		
A/Residues: 1-422 <V2>		
A/Cross-references: UNIPARC:UPI00000358B9; EMBL:U32324; NID:9975336; PIDN:AA83		
C/Genetics:		
A/Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2;		
C/Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homolog		
F/120-310/Domain: cytokine receptor homology <CR>		
Query Match 11.7%; Score 339.5; DB 2; Length 422;		
Best Local Similarity 29.1%; Pred. No. 1.7e-16;		
Matches 117; Conservative 48; Mismatches 180; Indels 57; Gaps 16		
Qy	2	LAVGCALLAALLAAPGAAL--APRCPAQEVARGVLITSLPGDSVTLTCGVEPEPNATVH 59
Db	1	MSSSCSGLSRVLVAVATALVASSPCPQAWGPPGVQYQPGRSVKLCCPGVTAGD--PVS 58
Qy	60	W-----VLKRPAGSHPSFSEWAGMRLLRLRSVLQHDGNGVSCYRA-GRPAGTVHLLVD 111
Db	59	WFRDGEPLKLGPD-----SGLGHLELVLAQADSTDEGTYICOTLDGALGGTVTLQG 110
Qy	112	VPPEEPQLSCFRKSPLSNVVCEWGPSTPSLTT-----KAVLLVRKFGNSPAEDFQE 163
Db	111	YPPARPVVSC-QAADYENFSCWSPQSISGLPTRYLTYSRKTKTVLGADSQRSPTG-PW 168
Qy	164	PCQYSQBSQKFSQCLAVPEGDS--SFYIVSMCVASSGVSKFSKTKTQTFQCGGILQPPPPAN 221
Db	169	PC-----PQDPLGAARCVVHGAEFWSQVRYINTEVNPLGAS-TRLIDVLSQSLIRPDPQ 223

Qy 329 TPQALTTNKDDDDNIL-PRDSANATSLPVERFGAGLVLGQFMPVPPGDSKDVAAPHROP 387
Db 326 DWSQG-----HGQQLAEAVVVAQEDSPAPARPSLOP 354

Search completed: September 7, 2006, 23:03:48
Job time : 43 secs

Qy 222 ITVTAVARNPRMLSVTQDDPHSWN-SSFYRLRFELRYRAERSKTFKTTMMVKDLQHHCVIH 280
Db 224 LRVESVPGYPRRLRASRTYPASWPCQPHFLKFLQYRPAQHAPAWSTVEPAGLEE--VIT 281

Qy 281 DAWSGLRHVQLRAQEGGQSEWSEPMAGTWTWES-----RSPPAENEVS 328
Db 282 DAVAGLPHAVRVSARDFLDAGTWTWSPGAWGTPTGTIPKBIAMGQLHTQPEVEPQVD 341

Qy 329 TPQALTTNKDDDDNIL-PRDSANATSLPVERFG-----AGLVLG 365
Db 342 SPAPRPSLQPHRLLDHRDSVEQVAVLASLGILSFLGLVAG 383

RESULT 15
I48343
interleukin-11 receptor alpha-chain precursor - mouse
N:Alternate names: cytokine type 1 receptor
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48343; S51619
R:Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle
Dev. Biol. 166, 521-542, 1994
A:Title: etl2, a novel putative type-1 cytokine receptor expressed during mouse embryoge
A:Reference number: I48343
A:Accession: I48343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
A:Cross-references: UNIPROT:Q64385; UNIPARC:UPI0000029ABF; EMBL:X74953; NID:G673437; PID
R:Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.;
EMBO J. 13, 4765-4775, 1994
A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high
A:Reference number: S51619; MUID:95045367; PMID:7957045
A:Accession: S51619
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432 <HIL>
A:Cross-references: UNIPARC:UPI0000029ABF; EMBL:U14412; NID:G576454; PIDN:AAA53248.1; PI
C:Genetics:
A:Gene: Et12/Il11
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C:Keywords: cytokine receptor
F:120-310/Domain: cytokine receptor homology <CRS>

Query Match 11.5%; Score 335; DB 2; Length 432;
Best Local Similarity 27.7%; Pred. No. 3.6e-16;
Matches 116; Conservative 43; Mismatches 162; Indels 98; Gaps 15;

Qy 2 LAVGCALLAALLAAPGAAL--APRRCPAQEVARGVLTSLPGDSVTLTCTCPGVEPDNATVH 59
Db 1 MSSSCSGLTRVLVAVATALVSSSSPCQAWGPPGVQGPGRPVMLCCPGV----- 51

Qy 60 WVLKRPAGSHPSRW-----AGMRILLRSVQLHDSGNVSCYRA-GRPAGT 105
Db 52 -----SAGT-FVSNFRDGRLLQGPSGIGHRLVLQAQVSDPEGTYVCTLDGVSGGM 104

Qy 106 VHLVVDVPEEPQLSCFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQNSPAEDFOE-- 163
Db 105 VTLKLGFPAPPEVSC-QADVENFSCTWSPQVSGLPTRYLTSYRKKTLPGAESQRESP 163

Qy 164 -----PCQYSESQKFSQCLAVPEGDS--SPYIVSMCVASSVSGSKFSKTQTFQGC----- 211
Db 164 STGFWPC----PQDPLEASRCVHGAEFWSEYRINVTENVPLGA-----STCLLDVR 211

Qy 212 --GILQDPDPANITVTVARNPRMLSVTQDDPHSW-NSSFYRLRFELRYRAERSKTFKTTW 268
Db 212 LQSLRPDPPOGLRVESVGGYPRRLHWSWTYPASMRQPHFLKFLRLQYRPAQHPAWST- 270

Qy 269 MVKDLQHHCVIHDAWSGLRHVVQLRAQEGGQSEWSEPMAGTWTWESRSPPAENEVS 328
Db 271 -VEPIGLEVITDAVAGLPHAVRVSARDFLDAGTWSAWSPEAWGTPTST----GPLQDEIP 325

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [7]
 RN NUCLEOTIDE SEQUENCE [MRNA] OF 313-365 (ISOFORM 2).
 RP MEDLINE=94333499; PubMed=8056053;
 RX Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
 RA Matsumoto A., Yamamoto M., Yamamoto N.;
 RA "Soluble interleukin-6 receptors released from T cell or
 RT granulocyte/macrophage cell lines and human peripheral blood
 RT mononuclear cells are generated through an alternative splicing
 RT mechanism.";
 RL Eur. J. Immunol. 24:1945-1948 (1994).
 [8]
 RP PARTIAL PROTEIN SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE
 RP BONDS.
 RX MEDLINE=99167486; PubMed=10065782; DOI=10.1074/jbc.274.11.7207;
 RA Cole A.R., Hall N.E., Treutlein H.R., Edes J.S., Reid G.E.,
 RA Moritz R.L., Simpson R.J.;
 RA "Disulfide bond structure and N-glycosylation sites of the
 RT extracellular domain of the human interleukin-6 receptor.";
 RL J. Biol. Chem. 274:7207-7215 (1999).
 [9]
 RN PROTEIN SEQUENCE OF 20-49, AND SUBCELLULAR LOCATION.
 RP MEDLINE=90010793; PubMed=2529343; DOI=10.1084/jem.170.4.1409;
 RX Novick D., Engelmann H., Wallach D., Rubinstein M.;
 RA "Soluble cytokine receptors are present in normal human urine.";
 RL J. Exp. Med. 170:1409-1414 (1989).
 [10]
 RN MUTAGENESIS.
 RP MEDLINE=93223711; PubMed=8467812;
 RX Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
 RA Taga T., Kishimoto T.;
 RA "Structure-function analysis of human IL-6 receptor: dissociation of
 RT amino acid residues required for IL-6-binding and for IL-6 signal
 RT transduction through gp130.";
 RL EMBO J. 12:1705-1712 (1993).
 [11]
 RP FUNCTION.
 RX PubMed=11017875;
 RA Martens A.S., Bode J.G., Heinrich P.C., Graeve L.;
 RA "The cytoplasmic domain of the interleukin-6 receptor gp80 mediates
 RT its basolateral sorting in polarized madin-darby canine kidney
 RT cells.";
 RL J. Cell Sci. 113:3593-3602 (2000).
 [12]
 RN FUNCTION, AND SUBCELLULAR LOCATION.
 RP PubMed=16270750; DOI=10.1016/j.ejcb.2005.06.001;
 RX Buk D.M., Renner O., Graeve L.;
 RA "Increased association with detergent-resistant membranes/lipid rafts
 RT of apically targeted mutants of the interleukin-6 receptor gp80.";
 RL Eur. J. Cell Biol. 84:819-831 (2005).
 [13]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 20-344.
 RP PubMed=12461182; DOI=10.1073/pnas.23243299;
 RX Varghese J.N., Moritz R.L., Lou M.-Z., Van Donkelaar A., Ji H.,
 RA Ivancic N., Branson K.M., Hall N.E., Simpson R.J.;
 RA "Structure of the extracellular domains of the human interleukin-6
 RT receptor alpha-chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15959-15964 (2002).

CC -!- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
 CC with low affinity, but does not transduce a signal. Signal
 CC activation necessitate an association with IL6ST. Activation may
 CC lead to the regulation of the immune response, acute-phase
 CC reactions and hematopoiesis.
 CC -!- FUNCTION: Low concentration of a soluble form of interleukin-6
 CC receptor acts as an agonist of IL6 activity.
 CC -!- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST.
 CC -!- INTERACTION:
 CC QNZ08:ARTS-1; NbExp=1; IntAct=EBI-299383, EBI-299412;
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC basolateral membrane. Secreted (isoform 2).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=long;
 CC IsoId=P08887-1; Sequence=displayed;
 CC Name=2; Synonyms=short;
 CC IsoId=SP001682; Sequence=VSP_001682, VSP_001683;
 CC -!- TISSUE SPECIFICITY: Isoform 2 is expressed in peripheral blood
 CC mononuclear cells and weakly found in urine and serum.
 CC -!- DOMAIN: The two fibronectin type-III-like domains, contained in
 CC the N-terminal part, form together a cytokine-binding domain.
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
 CC folding and thereby efficient intracellular transport and cell-
 CC surface receptor binding.
 CC -!- PTM: A short soluble form may also be released from the membrane
 CC by proteolysis.
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
 CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
 CC domain.
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; X12830; CAA31312.1; -; mRNA.
 CC EMBL; X58298; CAA41231.1; -; mRNA.
 CC EMBL; AK223582; BAB97302.1; -; mRNA.
 CC EMBL; AL162591; CAH72853.1; -; Genomic_DNA.
 CC EMBL; BC089410; AAH89410.1; -; mRNA.
 CC EMBL; S72848; AAC60635.1; -; mRNA.
 CC PIR; A41242; A41242.
 CC PDB; 1N26; X-ray; A=20-344.
 CC PDB; 1N2Q; Model; C/D=20-344.
 CC PDB; 1P9M; X-ray; C=115-315.
 CC IntAct; P08887; -.
 CC Ensembl; ENSG00000160712; Homo sapiens.
 CC HGNC; HGNC:6019; IL6R.
 CC MIM; 147880; gene.
 CC LinkHub; P08887; -.
 CC GO; GO:0005576; C:extracellular region; IDA.
 CC GO; GO:0005896; C:interleukin-6 receptor complex; TAS.
 CC GO; GO:0019899; F:enzyme binding; IPI.
 CC GO; GO:0004915; F:interleukin-6 receptor activity; TAS.
 CC GO; GO:0008283; P:cell proliferation; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 CC GO; GO:0007275; P:development; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC InterPro; IPR02996; Cytokn rcpt_B/G.
 CC InterPro; IPR03961; FN III.
 CC InterPro; IPR03530; Hempt_rcpt_L_F3.
 CC InterPro; IPR03599; Ig.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR03598; Ig_c2.
 CC InterPro; IPR013151; Immunoglobulin.
 CC Pfam; PF00041; fn3; 1.
 CC Pfam; PF00047; ig; 1.
 CC SMART; SM00060; FN3; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00408; IGC2; 1.
 CC PROSITE; PS0853; FN3; 1.
 CC PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.

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DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Alternative splicing; Direct protein sequencing;
Query Match 65.8%; Score 1917; DB 1; Length 468;
Best Local Similarity 96.8%; Pred. No. 9.8e-131;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALAAAPGAALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGCALLAALAAAPGAALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYRAERSKFTTWWVXDLOHHCYVHDHAWSLRHVVQLRAQEERFG 300
DB 241 PHSWNSFYRLRFELRYRAERSKFTTWWVXDLOHHCYVHDHAWSLRHVVQLRAQEERFG 300

QY 301 GEWSSEPEANGTPWTSERSPPAENEVSTPMQALTNKDDNILFRDSANATSLPVEFGA 360
DB 301 GEWSSEPEANGTPWTSERSPPAENEVSTPMQALTNKDDNILFRDSANATSLPVEFGA 360

QY 361 G-----LVLGG 366
DB 361 SVPLPTFLVAGG 372

RESULT 2
IL6RA PIG STANDARD; PRT; 467 AA.
AC 018796;
DT 01-DEC-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2000, sequence version 2.
DT 07-MAR-2006, entry version 49.
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=IL6R;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Morris K.R., Strom A.D.G.;
RT "Cloning and expression of biologically active porcine IL-6 receptor
RT alpha chain.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RW [2]
RP NUCLEOTIDE SEQUENCE [MRNA] OF 123-186.
RA Klir J.J., Matteri R.L.;
RT "Partial cDNA sequence of porcine interleukin 6 receptor.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Part of the receptor for Interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitates an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -!- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- TISSUE SPECIFICITY: Expressed in liver.
```

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CC -!- DOMAIN: The two fibronectin type-III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
DR EMBL; AF147881; AAF73109.1; -; mRNA.
DR EMBL; AF415116; AAB70916.1; -; mRNA.
DR HSPF; P08887; IN26.
DR SMR; O18796; 20-318.
DR InterPro; IPR002996; Cytokn_rcpt_B/G.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50853; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 467 Interleukin-6 receptor alpha chain.
FT /FTID=PRO 0000010897.
FT TOPO_DOM 20 365 Extracellular (Potential).
FT TRANSMEM 366 386 Potential.
FT TOPO_DOM 387 467 Cytoplasmic (Potential).
FT DOMAIN 20 112 Ig-like C2-type.
FT MOTIF 216 311 Fibronectin type-III.
FT MOTIF 303 307 WSXWS motif.
FT CARBOHYD 55 55 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 93 93 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 221 221 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 350 350 N-linked (GlcNAc...) (Potential).
FT DISULFID 25 193 By similarity.
FT DISULFID 47 96 By similarity.
FT DISULFID 121 132 By similarity.
FT DISULFID 165 176 By similarity.
SQ SEQUENCE 467 AA; 51067 MW; A2B0B884BF21C502 CRC64;

Query Match 50.5%; Score 1471; DB 1; Length 467;
Best Local Similarity 75.5%; Pred. No. 2.7e-98;
Matches 281; Conservative 27; Mismatches 58; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALAAAPGAALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
DB 1 MLAVGCALLAALAAAPGAALAPRRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120
DB 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPOL 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240
DB 181 PEGDSSFYIVSMCVASSVSGSKFTQTQGGCIGILQDPPANITVTAVARNPRLSVTWQD 240
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QY 241 PHSNWSFYRURFELRYRAERSKFTTMMVKDLQHCHVHDWGLRHVVQLRAQEERFG 300
Db 241 PPSNWSFYRLOFELRYRAERSKFTTMMVKELQHCHVHDWGLRHVVQLRAQEERFGH 300
QY 301 GEMSEWPEAMGTPTWTSRSPAESEVSTPMQALTTNKDDNIIILFRSANATSLPVEFGA 360
Db 301 GLMSEWQEVGTPTWTSRSPAESEVSTPMQALTTNKDDNIIILFRSANATSLPVDQSA 360
QY 361 G-----LVLGG 366
Db 361 SVPLPTFLVAGG 372

RESULT 3
IL6RA RAT
ID IL6RA RAT STANDARD; PRT; 462 AA.
AC P22273;
DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-FEB-1995, sequence version 2.
DT 07-MAR-2006, entry version 57.
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=IL6r;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Fischer 344; TISSUE=Liver;
RX MEDLINE=91060602; PubMed=2174054;
RA Baumann M., Baumann H., Fey G.H.;
RT "Molecular cloning, characterization and functional expression of the
RT rat liver interleukin 6 receptor.";
RL J. Biol. Chem. 265:19853-19862(1990).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
RA Gibson T.;
RL Unpublished observations (FEB-1995).
CC -!- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitate an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -!- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -!- DOMAIN: The two fibronectin type-III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -!- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -!- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC -----
CC EMBL: M58587; AAA41431.1; -; mRNA.
CC DR PIR: A37986; A37986.
CC DR HSSP: P08887; 1N26.
CC DR Ensembl: ENSRNOG00000020811; Rattus norvegicus.
CC DR RGD: 2902; 116r.
CC DR InterPro: IPR002996; Cytokn_rcpt_B/G.
CC DR InterPro: IPR003961; FN III.
CC DR InterPro: IPR003530; Hempt_rcpt_L_F3.
CC DR InterPro: IPR003599; Ig.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR013151; Immunoglobulin.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00409; IG_1.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS00853; FN3; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE: PS00835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 19 Interleukin-6 receptor alpha chain.
FT CHAIN 20 462 /FTID=PRO_000010898.
FT FT Extracellular (Potential).
FT FT Potential.
FT FT Cytoplasmic (Potential).
FT FT Ig-like C2-type.
FT FT Fibronectin type-III.
FT FT WSXWS motif.
FT FT Poly-Pro.
FT FT N-linked (GlcNAc...) (Potential).
FT FT N-linked (GlcNAc...) (Potential).
FT FT N-linked (GlcNAc...) (Potential).
FT FT N-linked (GlcNAc...) (Potential).
FT FT By similarity.
FT FT By similarity.
FT FT By similarity.
FT FT By similarity.
FT FT By similarity.
FT FT By similarity.
FT FT XPRWLKVSQDPPSGNSWDSYLLQFELRYRPVWSKX -> SL
FT FT VGSKSVGKTLSPGTQVTTCCNSSPDTLYGORT (in
FT FT Ref. 1).
SQ SEQUENCE 462 AA; 50401 MW; A4D6064CEDC0537D CRC64;

Query Match 34.2%; Score 994.5; DB 1; Length 462;
Best Local Similarity 51.9%; Pred. No. 1.3e-63;
Matches 195; Conservative 50; Mismatches 116; Indels 15; Gaps 5;

QY 1 MLAVGCALLAALAAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCTLLVALLAAPAVALVLGSCRALEVANGVTSLPGATVTLICPGKEAGNATHW 60
QY 61 VLKPAAGSHPSWAGMRLLRSVLQHDGNSYCVACRGPACTVHLLVDVPPPEPOL 120
Db 61 VY----SGSQSRENTTGTNTLVRAVQVNDTHYLCFLDDHLVGTVPLLVDPPEPKLS 116
QY 121 CFRKSPLSNVVCEWGPSTSLTTKALLVRKFNQSPAE-DFQSPCOVSOESQKFSCLA 179
Db 117 CFRKNPLVNAFCEWHGPSTSPPTTKAVMFARKINTNGKSDQFQVPCQVSQQLKSFCEVE 176
QY 180 VPGDSSFYIVSMCVASSVSGSKFTQTFCGCLQDPDPANITVTAVARNPRVLSVTWQ 239
Db 177 ILEGDKYHIVSLCVANSVGRSSHNVVFSQSLKMWQDPDPANLVSAIPGKPRMLKVSQ 236
QY 240 DPHSNWSFYRLAPELRYRAERSKFTTMMVKDLQHCHVHDWGLRHVVQLRAQEERFG 299
Db 237 DPESWDPSSYYLLOFELRYRPVWSKXFTVWPLQVAHQCVIHDALRGVHVQVQKGEF 296
QY 300 QGEMSEWPEAMGTPTW-TESRSPAESEVSTPMQALTTNKDDNIIILFRSANATSL---- 354
Db 297 IGOMSKWSPEVTGTPMLAEPRRTTPA-GIPGNPTQSVSEVDYDNHEDYQGSSTEATSLAPV 355
QY 355 ----PVDFGAGLVGG 366
Db 356 QGSSPIPLPTFLVAGG 371

RESULT 4
Q3URV7 MOUSE
ID Q3URV7 MOUSE PRELIMINARY; PRT; 459 AA.
AC Q3URV7;
DT 11-OCT-2005, integrated into UniProtKB/TREMBL.

```

DT 11-OCT-2005, sequence version 1.
 DT 21-FEB-2006, entry version 8.
 DE 0 day neonate cerebellum cDNA, RIKEN full-length enriched library,
 DE clone:C230098M17 product:interleukin 6 receptor, alpha, full insert
 DE sequence.
 GN Name=Il6ra;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Anweiler R., Aturaliya R.N., Bailey T.L.,
 RA Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukuhima T., Furuno M., Putaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hill D., Humnick L., Iacono M., Ikeo K., Iwama K., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakajima H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petkovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Sempile C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugitara K., Sultana R., Takenaka Y., Taki K.,
 RA Tannoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yananishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh T., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
[8]

RT NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Arakawa T., Carninci P., Fukuda S., Haehizume W., Hayashida K.,
RA Hori F., Iida J., Inamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,
RA Muramatsu M., Havaehizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK141197; BAE24580.1; -; mRNA.
DR MGI; MGI:105304; Il6ra.
DR GO; GO:0016021; C:integral to membrane; RCA.
DR InterPro; IPR002996; Cyt_kn_rcpt_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 50384 MW; 3575EBFC6AB8477 CRC64;

Query Match 33.1%; Score 963; DB 2; Length 459;
Best Local Similarity 50.9%; Pred. No. 2.4e-61;
Matches 191; Conservative 49; Mismatches 121; Indels 14; Gaps 5;
QY 1 MLAVGCALLAALLAALPAAGAAAPRCQAQVARGVLTSLPGDSVTLTCGPVEPDNATVHW 60
DB 1 MLTVGCTLLVALLAALPAVALVLSGRALVANGVTSLPGATVTLICPGEEAGNVTIHW 60
QY 61 VLRKPAAGHPSRWAGMGRLLLSVQLHDSNGVSCYRAGPAGTGHLLVDVPPPEPQLS 120
DB 61 VY----SGSQNRWTTTNTLVLRDVLQSLDGTGDLCSLNDHLVGTVPLLVDVPPPEPKLS 116
QY 121 CFRKSPLSNVVCEGPRSTPSLTTKAVLLVRKFKQNSPAE-DFOEPCOYSQESQKFSCLA 179
DB 117 CFRKNPLVNAICEWRPSTSPSTTKAVLLFAKKINTNGKSDFPVPCQYSQOLKSFSCQVE 176
QY 180 VPEGDSFPYIVCMVAVSGSKFSKFTOTFOCGILQDPDPANITVTAVARNPRLVSTWQ 239
DB 177 ILEGDKVYHIVSLCVANSVSGSKSHNEAFSLKMKVQDPDPANLVVSAIPGRPRLKVSQW 236
QY 240 DPHSWNSFYRLRFELRYAERSKTFTTMMVKDIQHHCVTHDWSGLRHVVQLRAQEFEG 299
DB 237 HPETWDSYLLQLQRLRYRVPWSKEFTVLLLPVAQYQCVIHDALRGKVKVQVVRGSELD 296
QY 300 QGENSENSPEAKGTPTWETSPRAENSVETPMQALTTNKDDNLTFRDSANATSL--PVE 357
DB 297 LGQENSESPVETGTPWIEPRTTPA-GILWNPQTQSVSDSANHEDQYESSTSEATSVLAPVQ 355
QY 358 FGAG-----LVLAG 366
DB 356 ESSNSLPTFLVAGG 370

RESULT 5
IL6RA MOUSE
ID IL6RA MOUSE STANDARD; PRT; 460 AA.
AC P22272;

DT 01-AUG-1991, integrated into UniProtKB/Swiss-Prot.
DT 01-AUG-1992, sequence version 2.
DE 07-MAR-2006, entry version 60.
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE (CD126 antigen).
GN Name=Il6ra; Synonyms=Il6r;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=BALB/c; TISSUE=Spleen;
RX MEDLINE=90278354; PubMed=2112585; DOI=10.1084/jem.171.6.2001;
RA Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,
RA Kishimoto T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A
RT particle gene product at its cytoplasmic domain. Its possible role in
RT plasmacytogenesis.";
RL J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C3H; TISSUE=Liver;
RA Fiorillo M.T., Ciliberto G., Dente L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Part of the receptor for interleukin 6. Binds to IL-6
CC with low affinity, but does not transduce a signal. Signal
CC activation necessitate an association with IL6ST. Activation may
CC lead to the regulation of the immune response, acute-phase
CC reactions and hematopoiesis.
CC -1- SUBUNIT: Hexamer of two molecules each of IL6, IL6R and IL6ST (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein.
CC -1- DOMAIN: The two fibronectin type-III-like domains contained in the
CC C-terminal part form together a cytokine-binding domain.
CC -1- DOMAIN: The WSWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding.
CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 3
CC subfamily.
CC -1- SIMILARITY: Contains 1 fibronectin type-III domain.
CC -1- SIMILARITY: Contains 1 Ig-like C2-type (immunoglobulin-like)
CC domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X51975; CAA36237.1; -; mRNA.
DR EMBL; X53802; CAA37810.1; -; mRNA.
DR PIR; JLO144; JLO144.
DR PIR; JLO145; JLO145.
DR HSP; P08887; IN26.
DR Ensembl; ENSMUSG0000027947; Mus musculus.
DR MGI; MGI:105304; Il6ra.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR002996; Cyt_kn_rcpt_B/G.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003530; Hempt_rcpt_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR013151; Immunoglobulin.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00853; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Membrane; Receptor; Signal;

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KW Transmembrane. 1
FT SIGNAL 20 460
FT FTID=PRO 0000010896.
FT Interleukin-6 receptor alpha chain.
FT Extracellular (Potential).
FT Potential.
FT TOPO_DOM 20 364
FT TRANSMEM 365 385
FT TOPO_DOM 386 460
FT DOMAIN 20 116
FT DOMAIN 213 308
FT MOTIF 300 304
FT COMBIDAS 404 408
FT CARBOHYD 32 32
FT CARBOHYD 55 55
FT CARBOHYD 150 190
FT DISULFID 25 190
FT DISULFID 47 92
FT DISULFID 117 128
FT DISULFID 162 173
FT CONFLICT 374 374
SQ SEQUENCE 460 AA; 50455 MW; F85C5906D08525C4 CRC64;

Query Match 32.7%; Score 953.5; DB 1; Length 460;
Best Local Similarity 50.8%; Pred. No. 1.2e-60;
Matches 191; Conservative 49; Mismatches 121; Indels 15; Gaps 6;

Qy 1 MLVGCALLAALAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCTPGVEPEDNATVHW 60
Db 1 MLTVGCTLLVALLAAPALVALVLSGCALEVANGTVTSLPGATVTLICPGKEAGNVTHW 60

Qy 61 VLKPAAGSHPSRMAGMGRLLRLSRVQLHDSGNTSCYRAGRPAGTVHLLVDVPEEPQLS 120
Db 61 VY----SGSQNRWTTTNTGLVLRDVLQSLSDTGLDCLNDHLVGVPLVLDVPEEPKLS 116

Qy 121 CFRKSPNVVCEWCPRTSPSLTKAVLLVRKFQNSPAE-DFQPCQYSQSKFSCOLA 179
Db 117 CFRKNPLNALCEWRSPSTPPTTKAVLFAKKINTNGSKDFQVPCQYSQSKFSCQVE 176

Qy 180 VPEGDSFYIVSMCVASVSGKFSKTQTFQGGILQPPDPPANITVTAVARNPRLSVTWQ 239
Db 177 ILEGDKVHYVSLCVANSVSGKSHNEAFSLKMWQPPDPPANLVSAIPGPRMLKVSQW 236

Qy 240 DPHSNMSFYRLRFELRYAERSKTFMTVMVKDLQHCVHDAMSLGRHVQLRAQEFEG 299
Db 237 HPETWDPSYLLQFLRYRPMVSKFTVLLLPVAQYQCVIHDALRGVHVQVVRGKBLD 296

Qy 300 QGEHSEWSPBANGTW-TESSRSPPAENEVSTPMQALTKDDNLLFRDSANATSL--PV 356
Db 297 LGQWSEWSPVETGTPIAEPRTPPA-GILWNPQTQVSDVSANHEDQYESSTEATSVLAPV 355

Qy 357 EFGAG-----LVLG 366
Db 356 QESSMSLPTFLVAGG 371

RESULT 6
IL6_HUMAN
ID IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231; Q9UCU2; Q9UCU4;
DT 13-AUG-1987, integrated into UniProtKB/Swiss-Prot.
DT 13-AUG-1987, sequence version 1.
DT 07-FEB-2006, entry version 75.
DE Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
DE (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation
DE factor) (CDF).
GN Name=IL6; Synonyms=IFNB2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
MEDLINE=87065033; PubMed=3491322;

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RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuuda T.,
RA Kashiwamura S., Nakajima K., Koyama K., Iwamatsu A., Tsunashima S.,
RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
RT "Complementary DNA for a novel human interleukin (BSF-2) that induces
RL B lymphocytes to produce immunoglobulin.";
RN Nature 324:73-76(1986).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88082664; PubMed=3500852;
RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuuda T.,
RA Nakai S., Kishimoto T.;
RT "Structure and expression of human B cell stimulatory factor-2 (BSF-
RT 2/IL-6) gene.";
RN EMBO J. 6:2939-2945(1987).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=07067433; PubMed=3538015;
RA May L.T., Helfgott D.C., Sehgal P.B.;
RT "Anti-beta-interferon antibodies inhibit the increased expression of
RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
RT structural studies of the beta 2 interferon involved.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
[4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87053818; PubMed=3023045;
RA Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
RT "Structure and expression of cDNA and genes for human interferon-beta-
RT 2, a distinct species inducible by growth-stimulatory cytokines.";
RL EMBO J. 5:2529-2537(1986).
[5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88089768; PubMed=3320204;
RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli.";
RL J. Immunol. 139:4116-4121(1987).
[6]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89391958; PubMed=2789513;
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells.";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
[7]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=87004683; PubMed=3758081;
RA Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
RA Piers W.;
RT "Structural analysis of the sequence coding for an inducible 26-kDa
RT protein in human fibroblasts.";
RL Eur. J. Biochem. 159:625-632(1986).
[8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89193317; PubMed=3266463;
RA Wong G., Witke-Giannotti J., Hewick R., Clark S., Ogawa M.;
RT "Interleukin 6: identification as a hematopoietic colony-stimulating
RT factor.";
RL Behring Inst. Mitt. 83:40-47(1988).
[9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93178270; PubMed=1291290;
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer.";
RL Zhonghua Zhong Liu Za Zhi 14:340-344(1992).
[10]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS SER-32 AND VAL-162.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-

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RT FHRC, Seattle, WA (URL: <http://pga.gs.washington.edu/>);
RL Submitted (JUN-2001) to the ENBL/GenBank/DBJ databases.
RN [11]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX TISSUE=Lung;
RA MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [12]
RP PROTEIN SEQUENCE OF 30-63.
RX MEDLINE=8915445; PubMed=3279116;
RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with lymphocyte-activating
RT factor activity: IL-1 beta and hybridoma growth factor (HGF).
RT Identification of leukocyte-derived HGF as IL-6.";
RL J. Immunol. 140:1534-1541 (1988).
RN [13]
RP PROTEIN SEQUENCE OF 30-50.
RX MEDLINE=90121567; PubMed=2610854;
RA Ming J.E., Cernetti C., Steinman R.M., Graneli-Piperno A.;
RT "Interleukin 6 is the principal cytolytic T lymphocyte differentiation
RT factor for thymocytes in human leukocyte conditioned medium.";
RL J. Mol. Cell. Immunol. 4:203-211 (1989).
RN [14]
RP PROTEIN SEQUENCE OF 30-40, AND GLYCOSYLATION.
RX MEDLINE=9135364; PubMed=1893960; DOI=10.1016/1043-4666(91)90018-9;
RA May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;
RT "Marked cell-type-specific differences in glycosylation of human
RT interleukin-6.";
RL Cytokine 3:204-211 (1991).
RN [15]
RP PROTEIN SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE
RP BOND.
RX MEDLINE=9515434; PubMed=7851440;
RA Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
RA Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond.";
RL Eur. J. Biochem. 227:573-581 (1995).
RN [16]
RP DISULFIDE BONDS.
RX MEDLINE=89286115; PubMed=2472117;
RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Disulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor.";
RL Arch. Biochem. Biophys. 272:144-151 (1989).
RN [17]
RP MUTAGENESIS.
RX MEDLINE=91243808; PubMed=2037043; DOI=10.1016/0014-5793(91)90491-K;
RA Luetticken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an alpha-helical
RT structure of the C-terminus for biological activity of human IL-6.";
RL FEBS Lett. 282:265-267 (1991).

4
RN [18]
RP STRUCTURE BY NMR.
RX MEDLINE=96134845; PubMed=8555185; DOI=10.1021/bi951949e;
RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy.";
RL Biochemistry 35:273-281 (1996).
RN [19]
RP STRUCTURE BY NMR.
RX MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933;
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6.";
RL J. Mol. Biol. 268:468-481 (1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling.";
RL EMBO J. 16:989-997 (1997).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- PFM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- DATABASE: NAME=R&D Systems' cytokine mini-reviews: IL6;
CC WWW="http://www.rndsystems.com/asp/q_sitebuilder.asp?bodyId=208".
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; X04430; CAA28026.1; -; mRNA.
DR EMBL; M14584; AAA52728.1; -; mRNA.
Query Match 32.5%; Score 947.5; DB 1; Length 212;
Best Local Similarity 95.0%; Pred. No. 1.2e-60;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
QY 355 PVRFAG--LVIGQF--MPVPPGDSKDVAAHPHQPTSSERIDKQRYILDGIALRKE 411
DB 11 PVAFSLGLLVLPAAFPAPVPPGDSKDVAAHPHQPTSSERIDKQRYILDGIALRKE 70
QY 412 TCNKNSSCESSKEALAENNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQ 471
DB 71 TCNKNSSCESSKEALAENNLNLPKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYLQ 130
QY 472 NRFESEBEQARAVQMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMT 531
DB 131 NRFESEBEQARAVQMSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLQANQWLODMT 190
QY 532 THILRSFKFLOSSLRALQRM 553
DB 191 THILRSFKFLOSSLRALQRM 212
RESULT 7
Q75MH2_HUMAN
ID Q75MH2_HUMAN PRELIMINARY; PRT; 212 AA.
AC Q75MH2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 7.
DE Hypothetical protein IL6 (Interleukin 6) (Interferon, beta 2).
GN Name=IL6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
 RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
 RA Fowell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
 RA Kozlowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
 RA Tin-Wollam A.-M., Abbott A., Minx P., Maupin R., Strommatt C.,
 RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7";
 RL Nature 424:157-164(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Haekenson W., Nguyen C., Yeakum M.;
 RT "The sequence of Homo sapiens BAC clone RP11-240H8.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [5]
 NUCLEOTIDE SEQUENCE.
 RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RT "Cloning of human full-length CDSs in BD Creator (TM) System Donor
 RT vector.";
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 RN [6]
 NUCLEOTIDE SEQUENCE.
 RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AC073072; AAS07539.1; -; Genomic DNA.
 DR EMBL; BT019748; XAV38553.1; -; mRNA.
 DR EMBL; BT019749; XAV38554.1; -; mRNA.
 DR EMBL; CR450296; CAG29292.1; -; mRNA.
 DR SMR; Q75MH2; 47-212.
 DR Ensembl; ENSG00000136244; Homo sapiens.
 DR GO; GO:0005615; C:extracellular space; ISS.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
 DR GO; GO:0007267; P:cell-cell signaling; ISS.
 DR GO; GO:0006959; P:humoral immune response; ISS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR PANTHER; PTHR11457; Interleukin_6; 1.
 Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 212 AA; 23718 MW; 1FIEDIFE1B734079 CRC64;
 Query Match 32.5%; Score 947.5; DB 2; Length 212;
 Best Local Similarity 95.0%; Pred. NO. 1.2e-60;
 Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;
 QY 355 PVEFCAG--IVLGGQF-MPVPPGDSKDVAAAPHRQPLTSSSRIDKQIRVILDGISALRKE 411
 DB 11 PVAFSLGLLVLPAAFPAPVPFGDSKDVAAAPHRQPLTSSSRIDKQIRVILDGISALRKE 70
 QY 412 TCNKSNNMCSSKEALAEANNLNLPMKAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEVLIQ 471
 DB 71 TCNKSNNMCSSKEALAEANNLNLPMKAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEVLIQ 130
 QY 472 NRPSSSEQARAVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQWLODMT 531
 DB 131 NRPSSSEQARAVQMTKVLIOFLQKAKNLDATTPDPTTNASLLTKLQAOQWLODMT 190
 QY 532 THILRSKPEFLQSSLRALRQM 553
 DB 191 THILRSKPEFLQSSLRALRQM 212
 RESULT 8
 IL6_MACFA STANDARD; PRT; 212 AA.
 ID IL6 MACFA
 AC P79341;
 DT 15-JUL-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAY-1997, sequence version 1.
 DT 07-FEB-2006, entry version 35.
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_taxid=9541;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Tateami M.;
 RT "Molecular cloning and expression of cynomolgus monkey interleukin-
 RT 6".
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted protein.
 CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC -----
 DR EMBL; AB000554; BAA19148.1; -; mRNA.
 DR HSSP; P05231; IL6.
 DR SMR; P79341; 47-212.
 DR InterPro; IPR012351; Cytokine_4_hlx.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR PANTHER; PTHR11457; Interleukin_6; 1.
 Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN_6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.

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FT SIGNAL      1 27 Potential.
FT CHAIN       28 212 Interleukin-6.
FT CARBOHYD    73 73 /FTid=PRO.0000015584.
FT CARBOHYD    73 73 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD    72 172 N-linked (GlcNAc... ) (Potential).
FT DISULFID    72 78 By similarity.
FT DISULFID    101 111 By similarity.
SQ SEQUENCE    212 AA; 23654 MW; CF8173FCBF080389 CRC64;

Query Match      31.5%; Score 916.5; DB 1; Length 212;
Best Local Similarity 92.1%; Pred. No. 2.1e-58;
Matches 186; Conservative 3; Mismatches 10; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGSDSKDVAAPHQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSLGLLLVLPAAFPAPVLPVPGSDSKDVAAPHQPLTSSERIDKHIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOSGFNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNRSNNCESSKEALAENNLNPKMAEKDGCFOSGFNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRFESSEQARAVQMSTKVLIQFLQKAKNLDATTDPPTNASLLTKLQANQWLODMT 531
Db 131 NRFESSEQARAVQMSTKVLIQFLQKAKNLDATTPEPTNASLLTKLQANQWLODMT 190
Qy 532 THLILRSFKFQSSLRALRQM 553
Db 191 THLILRSFKFQSSLRALRQM 212

RESULT 9
IL6_MACTH
ID IL6_MACTH STANDARD; PRT; 212 AA.
AC Q5I6E3;
DT 12-APR-2005, integrated into UniProtKB/Swiss-Prot.
DT 15-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca thibetana (Pare David's macaque) (Tibetan macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=54602;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Wei K., Zou F.D., Xia S., Pan J., Yue B.S.;
RT "Molecular cloning and characterization of the interleukin 6 (IL6) gene from Tibetan macaque (Macaca thibetana) and its expression in Escherichia coli.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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EMBL: AY849928; AAJ33962.1; -; mRNA.
DR SRR; Q5I6E3; 47-212.
DR InterPro; IPR012351; Cytokine_4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.

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DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL      1 27 Potential.
FT CHAIN       28 212 Interleukin-6.
FT CARBOHYD    73 73 /FTid=PRO.0000015586.
FT CARBOHYD    72 172 N-linked (GlcNAc... ) (Potential).
FT DISULFID    72 78 N-linked (GlcNAc... ) (Potential).
FT DISULFID    101 111 By similarity.
SQ SEQUENCE    212 AA; 23626 MW; D0916CF3AF0B039E CRC64;

Query Match      31.3%; Score 912.5; DB 1; Length 212;
Best Local Similarity 91.6%; Pred. No. 4.1e-58;
Matches 185; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGSDSKDVAAPHQPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSLGLLLVLPAAFPAPVLPVPGSDSKDVAAPHQPLTSSERIDKHIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOSGFNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNRSNNCESSKEALAENNLNPKMAEKDGCFOSGFNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRFESSEQARAVQMSTKVLIQFLQKAKNLDATTDPPTNASLLTKLQANQWLODMT 531
Db 131 NRFESSEQARAVQMSTKVLIQFLQKAKNLDATTPEPTNASLLTKLQANQWLODMT 190
Qy 532 THLILRSFKFQSSLRALRQM 553
Db 191 THLILRSFKFQSSLRALRQM 212

RESULT 10
IL6_MACMU
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P5I494;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 35.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
RL J. Immunol. 155;3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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EMBL: L26028; AAA99978.1; -; mRNA.
DR HSP; P05231; IALU.
DR SRR; P5I494; 47-212.
DR InterPro; IPR012351; Cytokine_4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.

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DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PR004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 212 Interleukin-6.
FT CARBOHYD 73 73 /FTID=PRO 0000015585.
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 N-linked (GlcNAc...) (Potential).
FT DISULFID 101 111 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCAD CRC64;

Query Match 31.2%; Score 908.5; DB 1; Length 212;
Best Local Similarity 91.1%; Pred. No. 7.9e-58;
Matches 184; Conservative 5; Mismatches 10; Indels 3; Gaps 2;

QY 355 PVEFGAG--LVLGQGF-MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 411
DB 11 PVAFSLGLLVLPAPFAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 70

QY 412 TCNKNMCESSKEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEPEVYLEYIQ 471
DB 71 TCNRSNMCESSKEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEPEVYLEYIQ 130

QY 472 NRFESSEQARAVQSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 531
DB 131 NRFESSEQARAVQSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 190

QY 532 THILRSFKFLOSSLRALQRM 553
DB 191 THILRSFKFLOSSLRALQRM 212

RESULT 11
O97540 AOTNA PRELIMINARY; PRT; 209 AA.
AC O97540;
DT 01-MAY-1999, integrated into UniProtKB/TrEMBL.
DT 01-MAY-1999, sequence version 1.
DE 21-FEB-2006, entry version 25.
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]_TaxID=37293;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez B.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey";
RL Immunogenetics 54:645-653(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC
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CC
CC -----
CC EMBL; AF014510; AAD01536.1; -; mRNA.
CC HSSP; P05231; 1ALU.
CC SMR; O97540; 47-209.
CC GO; GO:0005615; C:extracellular space; ISS.
CC GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; ISS.
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DR GO; GO:0007267; P:cell-cell signaling; ISS.
DR GO; GO:0006959; P:humoral immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 212 Interleukin-6.
FT CARBOHYD 73 73 /FTID=PRO 0000015585.
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 N-linked (GlcNAc...) (Potential).
FT DISULFID 101 111 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23728 MW; 4130DFE0CF0BCAD CRC64;

Query Match 31.2%; Score 907.5; DB 2; Length 209;
Best Local Similarity 92.0%; Pred. No. 9.2e-58;
Matches 183; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

QY 355 PVEFGAG--LVLGQGF-MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE 411
DB 11 PVAFSLGLLVMPAPFAPVPPGEDSKDVAAPHROPLTSTEQIDKHIRYILDGIALRKE 70

QY 412 TCNKNMCESSKEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEPEVYLEYIQ 471
DB 71 TCNKNMCESSKEALAENNLNLPKMAEKDGCQSGFNEETCLVKIITGLLEPEVYLEYIQ 130

QY 472 NRFESSEQARAVQSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 531
DB 131 NRFESSEQARAVQSTKVLIOFLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 190

QY 532 THILRSFKFLOSSLRAL 550
DB 191 THILRSFKFLOSSLRAL 209

RESULT 12
IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 37.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]_TaxID=9531;
RP NUCLEOTIDE SEQUENCE [mRNA].
RC STRAIN=FUJ;
RX MEDLINE=9003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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CC
CC -----
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DR EMBL; L26032; AAA99972.1; -; mRNA.
DR HSSP; P05231; IALU.
DR SMR; P46650; 47-212.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 31.1%; Score 904.5; DB 1; Length 212;
Best Local Similarity 90.6%; Pred. No. 1.6e-57;
Matches 183; Conservative 5; Mismatches 11; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 411
Db 11 PVAFSLGLLLVLPAAFPAPVLPAGEDSKDVAAPHSQPLTSSERIDKHIRYILDGIALRKE 70

Qy 412 TCNKSNCSSKEALAENNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQ 471
Db 71 TCNRSNMCDSSTKEALAENNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQ 130

Qy 472 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 531
Db 131 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 190

Qy 532 THILRSFKFQSSSLRALRQM 553
Db 191 THILRSFKFQSSSLRALRQM 212

RESULT 13
IL6_SAISC
AC OBMKH0;
DT 23-NOV-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Cebinae; Saimiri.
OX NCBI_TaxID=9521;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA Heraud J.M., Laverne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel
RL monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RC Immunogenetics 54:20-29(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted protein.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
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DR EMBL; AF294757; AAK92044.1; -; mRNA.
DR HSSP; P05231; IL6.
DR SMR; OBMKH0; 47-212.
DR InterPro; IPR012351; Cytokine 4 hlx.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR PANTHER; PTHR11457; Interleukin_6; 1.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 160 160 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
SQ SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;

Query Match 27.8%; Score 810.5; DB 1; Length 212;
Best Local Similarity 83.2%; Pred. No. 1.1e-50;
Matches 168; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Qy 355 PVFEGAG--LVLGQGF-MPVPPGDSKDVAAPHRQPLTSSERIDKQIRYILDGIALRKE 411
Db 11 PVAFSLGLLLVMPAAPPAPVTLGEDSKVAAPNRQLTSTERIDKHIRYILDGIALRKE 70

Qy 412 TCNKSNCSSKEALAENNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQ 471
Db 71 ICNKSNCSSKEALAENNLPMKAEKDCGFCGSGFNEETCLVKIITGLLEFEVYLEYQ 130

Qy 472 NREFSSEQARAVQMSTKVLQIQLQKAKNLDAITTPDPTTNASLLTKLAQNQLQDMT 531
Db 131 NREFSSEQARAVQMSTKGLIQSLQKAKNLSAIAITPDPAITNASLLTKLAQNQLQDMT 190

Qy 532 THILRSFKFQSSSLRALRQM 553
Db 191 THILRSFKFQSSSLRALRQM 212

RESULT 14
Q9TTH3_AOTLE
ID Q9TTH3_AOTLE PRELIMINARY; PRT; 209 AA.
AC Q9TTH3;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 21-FEB-2006, entry version 24.
DE Interleukin-6 (fragment).
GN Name=IL-6;
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aotinae; Aotus.
OX NCBI_TaxID=43147;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey.";
RC Immunogenetics 54:645-653(2002).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and

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CC      plasmacytoma growth, it induces nerve cells differentiation, in
CC      hepatocytes it induces acute phase reactants (By similarity).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF097323; AAF21298.1; -, mRNA.
DR      HSSP; P05231; 1ALU.
DR      SMR; Q9TH3; 47-209.
DR      GO; GO:0005615; C:extracellular space; ISS.
DR      GO; GO:0005138; F:interleukin-6 receptor binding; ISS.
DR      GO; GO:0007126; P:cell surface receptor linked signal transdu. .; ISS.
DR      GO; GO:0007267; P:cell-cell signaling; ISS.
DR      GO; GO:0006959; P:humoral immune response; ISS.
DR      GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR      GO; GO:0008284; P:positive regulation of cell proliferation; ISS.
DR      InterPro; IPR012351; Cytokine_4_hlx.
DR      InterPro; IPR003573; IL6_MGF_GCSF.
DR      InterPro; IPR003574; Interleukin_6.
DR      PANTHER; PTHR11457; Interleukin_6; 1.
DR      Pfam; PF00489; IL6; 1.
DR      PRINTS; PR00433; IL6GCSFMGF.
DR      PRINTS; PR00434; INTERLEUKIN6.
DR      ProDom; PD004356; Interleukin_6; 1.
DR      SMART; SM00126; IL6; 1.
DR      PROSITE; PS00254; INTERLEUKIN_6; 1.
KW      Acute phase.
KW      Acute phase.
FT      NON_TER 1
FT      NON_TER 209
SQ      SEQUENCE 209 AA; 23116 MW; A0A3DFAA4BF560CC CRC64;

      Query Match      27.8%; Score 808.5; DB 2; Length 209;
      Best Local Similarity 83.9%; Pred. No. 1.5e-50;
      Matches 167; Conservative 10; Mismatches 19; Indels 3; Gaps 2;

QY      355 PVEFGAG--LVLGQF-MVPFGEDSKDVAAPHROPLTSSERIDKQIYILDGIALRKE 411
DB      11 PVAFSLGULLVMPAPFAPVPLGEDSKVAAPNRQLLTSTEQIDKHRYILEGIALRKE 70

QY      412 TCKNSNMCESSKEALAEANLNLPKVAEKDGGCFQSGFNEETCLVKIITGLLEFEVLEYLQ 471
DB      71 ICDKSNMCESSKEALAEANLNLPKVAEKDGGCFQSGFNEETCLVKIITGLLEFEVLEYLQ 130

QY      472 NRFESSEQAAVQSTKVLQFLQKAKNLDATTPDPTTNASLLTKLQAOQNWLODMT 531
DB      131 NRFESSEQAAVQSTKGLQSLQKAKNLSAIAITPDPTNASLLMKLQAOQNWLODMT 190

QY      532 THLILRSKFELQSSLRAL 550
DB      191 THLILRSKFELQSSLRAL 209

RESULT 15
QSDW05 CHICK
ID      QSDW05_CHICK PRELIMINARY; PRT; 445 AA.
AC      QSDW05;
DT      29-MAR-2005, integrated into UniProtKB/TrEMBL.
DT      29-MAR-2005, sequence version 1.
DT      07-MAR-2006, entry version 8.
DE      Interleukin-6 receptor alpha chain precursor.
GN      Name=il6ra;
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      PubMed=16153708; DOI=10.1016/j.j.dci.2005.05.007;
RA      Nishimichi N., Kawashima T., Hojo S., Horiuchi H., Furusawa S.,
RA      Matsuda H.;
RT      "Characterization and expression analysis of a chicken interleukin-6
RT      receptor alpha."
```

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RL      Dev. Comp. Immunol. 30:419-429(2006).
CC      -|- SUBUNIT: Heterotrimer of the alpha chain, LIIR and IL6ST (By
CC      similarity).
CC      -|- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC      similarity).
CC      -|- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC      folding and thereby efficient intracellular transport and cell-
CC      surface receptor binding (By similarity).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AB175664; BA090557.1; -, mRNA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      InterPro; IPR002996; Cytkn rcpt_B/G.
DR      InterPro; IPR003961; FN_III.
DR      InterPro; IPR003530; Hempt_rcpt_L_F3.
DR      InterPro; IPR003599; IG.
DR      InterPro; IPR07110; IG-like.
DR      InterPro; IPR013151; Immunoglobulin.
DR      Pfam; PF00041; fn3; 1.
DR      Pfam; PF00047; Ig; 1.
DR      Pfam; PF07686; V-set; 1.
DR      SMART; SM00060; FN3; 1.
DR      SMART; SM00409; IG; 1.
DR      PROSITE; PS0853; FN3; 1.
DR      PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR      PROSITE; PS0835; IG_Like; 1.
KW      Immunoglobulin domain; Membrane; Receptor; Repeat; Signal;
KW      Transmembrane.
FT      SIGNAL 1 20 Potential.
FT      CHAIN 21 445 Potential.
SQ      SEQUENCE 445 AA; 48827 MW; BIA90D89BD2776D9 CRC64;

      Query Match      23.0%; Score 670; DB 2; Length 445;
      Best Local Similarity 41.0%; Pred. No. 4.8e-40;
      Matches 159; Conservative 51; Mismatches 118; Indels 60; Gaps 12;

QY      8 LLAALLAAGAAALAP-RRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHWLRKPA 66
DB      8 LRAALLLTAAASSAPRRRCGPVALPQDTVLGRPGANVTLCCREREP-PNGTVLWSGRRRA 66

QY      67 AGHPSRWAGMRILLRLSLVOLHDSGNYSVCYRACRAGTCTVLLVDVPPPEPOLSCFRKSP 126
DB      67 LGG-----GNALLGLRPEDAGRYSCHLGHGHTLTVRLLEVEEPPEPHVSCSRSH 118

QY      127 LSNVVCWGPRTSPSLTTKAVL-LVRKFNQSPAEDEFQPCQYSQBSQKFCOLAYPEG-- 183
DB      119 DKDVLCEWRPRASPAPGTRAVLWMKRFTMENAT--EQRCHFYSAAQKFCVKVPPGTD 176

QY      184 DSSFYIVSMCVASSVGSKFSTQTQGGILOPPPPANITVTAVARNRWLSVTWQDPHS 243
DB      177 DTKALVWSVCVSSRAGSAAEDRIFTLNGILKPPPLNVTVEAVERSPQLCVRWSYPPS 236

QY      244 WNSSFYRLRFLRYRAERSKTFT-----TMMVKDLQHCCHVDHAWGLRHVQLRAQE 296
DB      237 WDPFYRLRFQVRYRPEPAPFTQVDQVTRTWL-----DIRDAWRGMRHVQVRAQE 288

QY      297 EFGQGEWSEWSPAMGTPTWTSRSPPAENESTPMAQLTNNKDDNILFRDSANATSLPV 356
DB      289 EFGHGAMSEWSEAVGTPTWTFRTDVTENGLSQFPA-----EDD-----PY 330

QY      357 EFGAGLVLGQGFMPVPP---GEDSKDVA 381
DB      331 GYGATL-----PPELFGDDTADDA 349

Search completed: September 7, 2006, 23:03:01
Job time : 304 secs
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10/11/18

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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:03:15 ; Search time 49 Seconds
(without alignments)
987.846 Million cell updates/sec

Title: US-09-462-416A-13
Perfect score: 2912
Sequence: 1 MLAVGCALLAALLAAPGAAL.....LILSRKFELQSSLRALROM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pdp.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pdp.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pdp.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pdp.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCUS_COMB.pdp.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pdp.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1927.5	66.2	592	2	US-09-313-942-8
2	1927.5	66.2	592	2	US-10-282-162-8
3	1917	65.8	468	2	US-08-795-473B-5
4	1917	65.8	468	2	US-09-439-856-5
5	1917	65.8	468	2	US-09-949-016-5959
6	1917	65.8	468	7	5171840-2
7	1917	65.8	468	7	5480796-2
8	1910	65.6	360	2	US-09-313-942-15
9	1910	65.6	360	2	US-10-282-162-15
10	1852	63.6	344	7	5171840-7
11	1852	63.6	344	7	5480796-7
12	1789	61.4	1158	2	US-09-313-942-26
13	1789	61.4	1158	2	US-10-282-162-26
14	1783	61.2	1168	2	US-09-313-942-24
15	1783	61.2	1168	2	US-10-282-162-24
16	1741	59.8	323	7	5171840-6
17	1741	59.8	323	7	5480796-6
18	1683	57.8	315	2	US-09-313-942-16
19	1683	57.8	315	2	US-10-282-162-16
20	1479	50.8	388	2	US-09-949-016-9852
21	1388	47.7	386	7	5171840-5
22	1388	47.7	386	7	5480796-5
23	1153	39.6	210	2	US-09-043-785-1
24	951.5	32.7	232	2	US-09-949-016-10315
25	950	32.6	201	7	5171840-11
26	947.5	32.5	212	1	US-08-792-019B-9

27	947.5	32.5	212	2	US-08-988-819-9	Sequence 9, Appli
28	947.5	32.5	212	2	US-09-016-534-9	Sequence 9, Appli
29	947.5	32.5	212	2	US-08-097-869-7	Sequence 7, Appli
30	947.5	32.5	212	2	US-08-795-473B-6	Sequence 6, Appli
31	947.5	32.5	212	2	US-09-230-637-45	Sequence 45, Appli
32	947.5	32.5	212	2	US-09-230-371A-27	Sequence 27, Appli
33	947.5	32.5	212	2	US-09-439-856-6	Sequence 6, Appli
34	947.5	32.5	212	2	US-09-462-941-13	Sequence 13, Appli
35	947.5	32.5	212	7	5510472-2	Patent No. 5510472
36	945	32.5	317	2	US-08-469-318-145	Sequence 145, App
37	945	32.5	317	2	US-08-468-609A-145	Sequence 145, App
38	945	32.5	317	2	US-08-446-872A-145	Sequence 145, App
39	945	32.5	317	2	US-08-762-227A-145	Sequence 145, App
40	945	32.5	317	5	PCT-US95-01185-145	Sequence 145, App
41	939.5	32.3	212	2	US-09-487-792-14	Sequence 14, Appli
42	939.5	32.3	212	2	US-09-908-594-14	Sequence 14, Appli
43	939	32.3	185	1	US-08-716-317-7	Sequence 7, Appli
44	934	32.1	184	1	US-08-567-047-2	Sequence 2, Appli
45	934	32.1	184	1	US-08-567-048-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-313-942-8
; Sequence 8, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-8

Query Match	66.2%	Score	1927.5	DB	2	Length	592
Best Local Similarity	72.8%	Pred. No.	6.9e-162				
Matches	391	Conservative	17	Mismatches	56	Indels	73
Gaps	8						
Qy	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLT	CPGVEPEDNATVHW	60			
Db	1	MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLT	CPGVEPEDNATVHW	60			
Qy	61	VLKPAAGSHPSRWAGMGRLLRSVLHDSGNTSCYRAGRPAAGTAVHLLVDVPPPEPQLS	120				
Db	61	VLKPAAGSHPSRWAGMGRLLRSVLHDSGNTSCYRAGRPAAGTAVHLLVDVPPPEPQLS	120				
Qy	121	CFKSPSLNVVCEWGPRTSLTKAVLLVRKFQNSPAEDFOEPQYQSOSKQFSCQLAV	180				
Db	121	CFKSPSLNVVCEWGPRTSLTKAVLLVRKFQNSPAEDFOEPQYQSOSKQFSCQLAV	180				
Qy	181	PEGSSFFIIVSMCVASSVGSFKSKTQTQGGCIGILQDPDPANITVAVARNRWLSVTWQD	240				
Db	181	PEGSSFFIIVSMCVASSVGSFKSKTQTQGGCIGILQDPDPANITVAVARNRWLSVTWQD	240				
Qy	241	PHSWNSSFYRLRFELRYAERSKTTFTTMMVKDLQHCVHDAMSLGRHVQLRAQBEFQ	300				
Db	241	PHSWNSSFYRLRFELRYAERSKTTFTTMMVKDLQHCVHDAMSLGRHVQLRAQBEFQ	300				
Qy	301	GEWSEWSEPMGTPTWTSERSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVEFG	359				

Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVQDAG 360
Qy 360 -----AGLVILGQ-----FMPVPPGSDSKDVAAPHROPL-----TSSER 393
Db 361 EPKSCDKTHTCPAPAPPELLGGPSVFLPPKP-----KDTLMSRTPEVTCVVVDVSHED 415
Qy 394 IDKQIRYILDGI-----SALRKETCNKNCESSKEALAENNLN-----LPK 435
Db 416 PEVKFNWVDGVEVHNAKTKPREQYNSYRVSVLTVLHODWLNKKEYKCKVSNKALPA 475
Qy 436 MAEKDGCFCQSGFNEE-----TCLVKITGLLBEVYVLEYLQN 472
Db 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEMESN 529

RESULT 2
US-10-282-162-8
; Sequence 8, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-8

Query Match 66.2%; Score 1927.5; DB 2; Length 592;

Best Local Similarity 72.8%; Pred. No. 6.9e-162;

Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNVSCYRAGRPAGTIVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNVSCYRAGRPAGTIVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVFEG- 359
Db 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVQDAG 360
Qy 360 -----AGLVILGQ-----FMPVPPGSDSKDVAAPHROPL-----TSSER 393
Db 361 EPKSCDKTHTCPAPAPPELLGGPSVFLPPKP-----KDTLMSRTPEVTCVVVDVSHED 415
Qy 394 IDKQIRYILDGI-----SALRKETCNKNCESSKEALAENNLN-----LPK 435
Db 416 PEVKFNWVDGVEVHNAKTKPREQYNSYRVSVLTVLHODWLNKKEYKCKVSNKALPA 475

Qy 436 MAEKDGCFCQSGFNEE-----TCLVKITGLLBEVYVLEYLQN 472
Db 476 PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEMESN 529

RESULT 3

US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858
; GENERAL INFORMATION:

; APPLICANT: Galun, Eithan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
US-08-795-473B-5

Query Match 65.8%; Score 1917; DB 2; Length 468;

Best Local Similarity 96.8%; Pred. No. 4.1e-161;

Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNVSCYRAGRPAGTIVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLSRVQLHDSGNVSCYRAGRPAGTIVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEPQPCQYSQESQKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFQGGIILQPPPPANITVTAVARNRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKFTFTTMVKDLQHHCVIHDWGLRHVVQLRAQEFEGQ 300
Qy 301 GEWSEWPEAMGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVFEGA 360

Db 301 GEWSEWSPAMGTPWTESTRSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVLG 366

Db 361 SVPLPTFLVAGG 372

RESULT 4

US-09-439-856-5

; Sequence 5, Application US/09439856

; Patent No. 6410009

; GENERAL INFORMATION:

; APPLICANT: Galun, Eithan

; APPLICANT: Nahot, Orit

; APPLICANT: Blum, Herbert E.

; TITLE OF INVENTION: A Pharmaceutical Composition for Treating

; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Davidson, Davidson and Kappel, LLC

; STREET: 1140 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS-DOS EDITOR

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/439,856

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/795,473

; FILING DATE: 11-FEB-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Davidson, Clifford M.

; REGISTRATION NUMBER: 32,728

; REFERENCE/DOCKET NUMBER: 963.1007

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)-997-1028

; TELEFAX: (212)-997-1037

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 468 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

US-09-439-856-5

Query Match 65.8%; Score 1917; DB 2; Length 468;

Best Local Similarity 96.8%; Pred. No. 4.1e-161;

Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFIVSMCVASSVSGSKFTQTQGGCGILOPDPANITVTAVARNRWLSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVSGSKFTQTQGGCGILOPDPANITVTAVARNRWLSVTWOD 240

QY 241 PHSMNSSFYRLRFELRYAERSKFTTTWVKDLOHHCVIHDAWSGLRHVVQLRAQEEFGQ 300

Db 241 PHSMNSSFYRLRFELRYAERSKFTTTWVKDLOHHCVIHDAWSGLRHVVQLRAQEEFGQ 300

QY 301 *GEWSEWSPAMGTPWTESTRSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVEFGA 360

Db 301 GEWSEWSPAMGTPWTESTRSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVLG 366

Db 361 SVPLPTFLVAGG 372

RESULT 5

US-09-949-016-5959

; Sequence 5959, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5959

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-5959

Query Match

Best Local Similarity 65.8%; Score 1917; DB 2; Length 468;

Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGPAAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFIVSMCVASSVSGSKFTQTQGGCGILOPDPANITVTAVARNRWLSVTWOD 240

Db 181 PEGDSSFIVSMCVASSVSGSKFTQTQGGCGILOPDPANITVTAVARNRWLSVTWOD 240

QY 241 PHSMNSSFYRLRFELRYAERSKFTTTWVKDLOHHCVIHDAWSGLRHVVQLRAQEEFGQ 300

Db 241 PHSMNSSFYRLRFELRYAERSKFTTTWVKDLOHHCVIHDAWSGLRHVVQLRAQEEFGQ 300

QY 301 GEWSEWSPAMGTPWTESTRSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVEFGA 360

Db 301 GEWSEWSPAMGTPWTESTRSPPAENEVSTPMQALTTNKDDNNILFRDSANATSLPVDSS 360

QY 361 G-----LVLG 366

Db 361 SVPLPTFLVAGG 372

RESULT 6

5171840-2

; Patent No. 5171840

; APPLICANT: KISHIMOTO, TADAMITSU

```
; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
; STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 11
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
; LENGTH: 468
5171840-2

Query Match      65.8%; Score 1917; DB 7; Length 468;
Best Local Similarity 96.8%; Pred. No. 4.1e-161;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180

Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240

Qy 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300
Db 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300

Qy 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVEFGA 360
Db 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVEFGA 360

Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372

RESULT 7
5480796-2
; Patent No. 5480796
; APPLICANT: KISHIMOTO, TADAMITSU
; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN
; FOR HUMAN B CELL STIMULATORY FACTOR-2
; NUMBER OF SEQUENCES: 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/907,650
; FILING DATE: 02-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 298,694
; FILING DATE: 19-JAN-1989
; SEQ ID NO:2:
; LENGTH: 468
5480796-2

Query Match      65.8%; Score 1917; DB 7; Length 468;
Best Local Similarity 96.8%; Pred. No. 4.1e-161;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60

Qy 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
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Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300
Db 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300
Qy 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVEFGA 360
Db 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVEFGA 360
Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372

RESULT 8
US-09-313-942-15
; Sequence 15, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-15

Query Match 65.6%; Score 1910; DB 2; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.1e-160;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Db 1 MLAVGCALLAALLAAPGAALAPRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW 60
Qy 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLKPAAGSHPSRWAGMGRLLRLSLVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDEFQPCQYSQESKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSTQTQFGCGIILQPPPPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300
Db 241 PHSWNSFYRLRFLRYRAERSKTFTTMMVKDLQHHCVIHDAMSGLRHVVLRAQEFGQ 300
Qy 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVE 357
Db 301 GEWSEWSPAMGTPTWESRSPPAENEVSTPMQALTTNKDDNILLFRSANATSLPVE 357

RESULT 9
```

US-10-282-162-15

; Sequence 15, Application US/10282162

; Patent No. 6927044

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

; TITLE OF INVENTION: AND USING

; FILE REFERENCE: REG 203-B-US

; CURRENT APPLICATION NUMBER: US/10/282,162

; CURRENT FILING DATE: 2002-10-28

; PRIOR APPLICATION NUMBER: 09/787,835

; PRIOR FILING DATE: 1999-09-22

; PRIOR APPLICATION NUMBER: PCT/US99/22045

; PRIOR FILING DATE: 1999-09-22

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-282-162-15

Query Match 65.6%; Score 1910; DB 2; Length 360;

Best Local Similarity 99.4%; Pred. No. 1.1e-160;

Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

Db 1 MVAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

Db 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

QY 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILLPRDSANATSLPV 357

Db 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILLPRDSANATSLPV 357

RESULT 10

5171840-7

; Patent No. 5171840

; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL

; STIMULATORY FACTOR-2

; NUMBER OF SEQUENCES: 11

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/298,694

; FILING DATE: 19-JAN-1989

; SEQ ID NO: 7;

; LENGTH: 344

5171840-7

Query Match

Best Local Similarity 63.6%; Score 1852; DB 7; Length 344;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

Db 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

QY 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILL 344

Db 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILL 344

RESULT 11

5480796-7

; Patent No. 5480796

; APPLICANT: KISHIMOTO, TADAMITSU

; TITLE OF INVENTION: ANTIBODIES AGAINST THE RECEPTOR PROTEIN

; FOR HUMAN B CELL STIMULATORY FACTOR-2

; NUMBER OF SEQUENCES: 8

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/907,650

; FILING DATE: 02-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 298,694

; FILING DATE: 19-JAN-1989

; SEQ ID NO: 7;

; LENGTH: 344

5480796-7

Query Match

Best Local Similarity 63.6%; Score 1852; DB 7; Length 344;

Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

Db 1 MLAVGCALLAALLAAGGALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHW 60

QY 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

Db 61 VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

Db 181 PEGDSSFYIVSMCVASSVSGSKFTQTFGGCGILQDPDPANITVTAVARNRWLSVTWQD 240

QY 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

Db 241 PHSWNSFYRLRFELRYAERSKTFTTMMVKDLQHCYVHDAWSGLRHVVQLRAQEEFQ 300

QY 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILL 344

Db 301 GEWSWSPPEAMGTPWTSRSPPAENEVSTPMQALTTNKDDNILL 344

RESULT 12

US-09-313-942-26

; Sequence 26, Application US/09313942

; Patent No. 6472179

; GENERAL INFORMATION:

; APPLICANT: REGENERON PHARMACEUTICALS, INC.

```
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-26

Query Match      61.4%; Score 1789; DB 2; Length 1158;
Best Local Similarity 58.7%; Pred. No. 3.7e-149; Indels 144; Gaps 13;
Matches 379; Conservative 35; Mismatches 88;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEQFQPCQYQSOESQKSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEQFQPCQYQSOESQKSCQLAV 180
Qy 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVAVARNRWLSVTWQD 240
Db 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVAVARNRWLSVTWQD 240
Qy 241 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQ 300
Db 241 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQ 300
Qy 301 GEWSEWPEAMGTPTWESRSPAEVNEVSTPMQAL----- 334
Db 301 GEWSEWPEAMGTPTWESRSPAEVNEVSTPMQAL----- 334
Qy 335 -----TTNKDDNILFRDSANAT-----SLPVEFGAGLVGQGF 368
Db 361 EKCMDFYHNANYIVWKTNHTIPEQVYTIINRTASSVTFTDIASLNIQLTCNLTFCQL 420
Qy 369 MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE-----TC-----NKSNNC 419
Db 421 -----EQNVYGITIISGLPPEKPKNLSCTIVNEGKMKRC 453
Qy 420 E--SSKEALAEENLNLPK-----MAEKD---GC-----FOSGFNEETCL 453
Db 454 EWDGGRTHLETNTFLKSEWATHKPAACKAKRDTPTSCVDYSTVYFVNIWVWEAENAL 513
Qy 454 VKIITGLLEFEVYLEYLNQ-----RFSSESEQAQAVQMS-----TKVLIQFIQK 497
Db 514 GKVTSDHINFDPVYKVPKPNPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTK 573
Qy 498 KAKNLDAITPDPPTNASLLTKLQAOQWLODMTHLLILRSFKFEL 543
Db 574 DASTWSQIPPEDTASTRSFT-----VQD-----LKPFTTEYV 605
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RESULT 13

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US-10-282-162-26
; Sequence 26, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
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; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-26
```

Query Match 61.4%; Score 1789; DB 2; Length 1158;

```
Best Local Similarity 58.7%; Pred. No. 3.7e-149; Indels 144; Gaps 13;
Matches 379; Conservative 35; Mismatches 88;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Db 1 MVAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Db 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNVSCYRAGRPAGTVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEQFQPCQYQSOESQKSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTKAVLLVRKFNQSPAEQFQPCQYQSOESQKSCQLAV 180
Qy 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVAVARNRWLSVTWQD 240
Db 181 PEGDSSFFIVSMCVASSVSGSKFTQTQFGCGILQDPDPANITVAVARNRWLSVTWQD 240
Qy 241 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQ 300
Db 241 PHSWNSSFYRLRFLRYRAERSKFTTMMVKDLQHHCVIHDWAGSLRHVVQLRAQEFQ 300
Qy 301 GEWSEWPEAMGTPTWESRSPAEVNEVSTPMQAL----- 334
Db 301 GEWSEWPEAMGTPTWESRSPAEVNEVSTPMQAL----- 334
Qy 335 -----TTNKDDNILFRDSANAT-----SLPVEFGAGLVGQGF 368
Db 361 EKCMDFYHNANYIVWKTNHTIPEQVYTIINRTASSVTFTDIASLNIQLTCNLTFCQL 420
Qy 369 MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKE-----TC-----NKSNNC 419
Db 421 -----EQNVYGITIISGLPPEKPKNLSCTIVNEGKMKRC 453
Qy 420 E--SSKEALAEENLNLPK-----MAEKD---GC-----FOSGFNEETCL 453
Db 454 EWDGGRTHLETNTFLKSEWATHKPAACKAKRDTPTSCVDYSTVYFVNIWVWEAENAL 513
Qy 454 VKIITGLLEFEVYLEYLNQ-----RFSSESEQAQAVQMS-----TKVLIQFIQK 497
Db 514 GKVTSDHINFDPVYKVPKPNPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTK 573
Qy 498 KAKNLDAITPDPPTNASLLTKLQAOQWLODMTHLLILRSFKFEL 543
Db 574 DASTWSQIPPEDTASTRSFT-----VQD-----LKPFTTEYV 605
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RESULT 14

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US-09-313-942-24
; Sequence 24, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
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; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-24

Query Match      61.2%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 1.3e-148;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
Db |:|||||
Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db |:|||||
Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db |:|||||
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQCYSQESQKFSQCLAV 180
Db |:|||||
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQCYSQESQKFSQCLAV 180
Db |:|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGGILQDPDPANITTVAVARNRWLSVTWQD 240
Db |:|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGGILQDPDPANITTVAVARNRWLSVTWQD 240
Db |:|||||
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCHVHDAWSGLRHVVQLRAQEEFGQ 300
Db |:|||||
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPM 331
Db |:|||||
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPM 331
Db |:|||||
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Search completed: September 7, 2006, 23:04:45
Job time : 51 secs

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; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-24

Query Match      61.2%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 1.3e-148;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
Db |:|||||
Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db |:|||||
Qy 61 VLKPAAGSHPSRWAGMGRRLRLRSVQLHDSGNTSCYRAGRPAAGTVHLLVDVPPPEPQLS 120
Db |:|||||
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQCYSQESQKFSQCLAV 180
Db |:|||||
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFQEPQCYSQESQKFSQCLAV 180
Db |:|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGGILQDPDPANITTVAVARNRWLSVTWQD 240
Db |:|||||
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSTQTFQGGGILQDPDPANITTVAVARNRWLSVTWQD 240
Db |:|||||
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCHVHDAWSGLRHVVQLRAQEEFGQ 300
Db |:|||||
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHCHVHDAWSGLRHVVQLRAQEEFGQ 300
Db |:|||||
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPM 331
Db |:|||||
Qy 301 GEWSEWSPAMGTPWTSRSPPAENEVSTPM 331
Db |:|||||

RESULT 15
US-10-282-162-24
; Sequence 24, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-24

Query Match      61.2%; Score 1783; DB 2; Length 1168;
Best Local Similarity 99.7%; Pred. No. 1.3e-148;
Matches 330; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEPNATVHM 60
Db |:|||||
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11/11/11

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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:04:00 ; Search time 176 seconds
(without alignments)
1455.442 Million cell updates/sec

Title: US-09-462-416A-13
Perfect score: 2912
Sequence: 1 MLAVGCALLAALLAAGGAAL.....LILRSFKFLOSLRALRQM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2789	95.8	569	5	US-10-485-545A-14
2	1927.5	66.2	592	3	US-09-313-942-8
3	1927.5	66.2	592	3	US-09-313-942-8
4	1927.5	66.2	592	4	US-10-287-035-8
5	1927.5	66.2	592	4	US-10-282-162-8
6	1927.5	66.2	592	6	US-11-134-114-8
7	1917	65.8	468	4	US-10-247-463-12
8	1917	65.8	468	5	US-10-756-149-5377
9	1917	65.8	468	6	US-11-016-106-12
10	1910	65.6	360	3	US-09-313-942-15
11	1910	65.6	360	3	US-09-935-868-15
12	1910	65.6	360	4	US-10-282-035-15
13	1910	65.6	360	4	US-10-282-162-15
14	1910	65.6	360	6	US-11-134-114-15
15	1901	65.3	468	5	US-10-485-545A-11
16	1897	65.1	357	5	US-10-485-545A-13
17	1891	64.9	364	5	US-10-485-545A-10
18	1891	64.9	365	5	US-10-485-545A-12
19	1822.5	62.6	453	4	US-10-322-696-144
20	1789	61.4	1158	3	US-09-313-942-26
21	1789	61.4	1158	3	US-09-935-868-26
22	1789	61.4	1158	4	US-10-287-035-26
23	1789	61.4	1158	4	US-10-282-162-26
24	1789	61.2	1158	6	US-11-134-114-26
25	1783	61.2	1168	3	US-09-313-942-24
26	1783	61.2	1168	3	US-09-935-868-24
27	1783	61.2	1168	4	US-10-287-035-24

28	1783	61.2	1168	4	US-10-282-162-24	Sequence 24, Appl
29	1783	61.2	1168	6	US-11-134-114-24	Sequence 24, Appl
30	1683	57.8	315	3	US-09-313-942-16	Sequence 16, Appl
31	1683	57.8	315	3	US-09-935-868-16	Sequence 16, Appl
32	1683	57.8	315	4	US-10-282-035-16	Sequence 16, Appl
33	1683	57.8	315	4	US-10-282-162-16	Sequence 16, Appl
34	1683	57.8	315	6	US-11-134-114-16	Sequence 16, Appl
35	953.5	32.7	387	4	US-10-322-696-141	Sequence 141, Appl
36	953.5	32.7	460	4	US-10-247-463-13	Sequence 13, Appl
37	953.5	32.7	460	6	US-11-016-106-13	Sequence 13, Appl
38	952.5	32.7	266	6	US-11-043-788-194	Sequence 194, Appl
39	947.5	32.5	212	3	US-09-854-280-14	Sequence 14, Appl
40	947.5	32.5	212	3	US-09-854-208-14	Sequence 14, Appl
41	947.5	32.5	212	4	US-10-099-007A-3	Sequence 3, Appl
42	947.5	32.5	212	4	US-10-400-377-13	Sequence 13, Appl
43	947.5	32.5	212	4	US-10-400-708-13	Sequence 13, Appl
44	947.5	32.5	212	4	US-10-298-148-13	Sequence 13, Appl
45	947.5	32.5	212	4	US-10-440-464-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-485-545A-14
; Sequence 14, Application US/10485545A
; Publication No. US20050064558A1
; GENERAL INFORMATION:
; APPLICANT: University College Cardiff
; APPLICANT: University of Wales College of Medicine
; FILE OF INVENTION: A Fusion Protein
; FILE REFERENCE: P102803PCT
; CURRENT APPLICATION NUMBER: US/10/485, 545A
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: 0119015.6
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 14
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-6 fusion protein
US-10-485-545A-14

Query Match	95.8%	Score	2789	DB	5	Length	569
Best Local Similarity	96.1%	Pred. No.	9.4e-212				
Matches	539	Conservative	0	Mismatches	12	Indels	10
Gaps	3						
QY	1	MLAVGCALLAALLAAGGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60				
DB	1	MLAVGCALLAALLAAGGAALAPRRCPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW	60				
QY	61	VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS	120				
DB	61	VLKPAAGSHPSRWAGMGRLLRLRSVQLHDSGNYSCYRAGRPAAGTVHLLVDVPPPEPQLS	120				
QY	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQQLAV	180				
DB	121	CFRKSPLSNVCEWGPRTSLTTKAVLLVRKFNQSPAEEDFOEPCQYSESQKFSQQLAV	180				
QY	181	PEGDSFFIVSMCVASSVSGSKFSTOTFGCGILQDPDPANITVTAVARNRWLSVTWOD	240				
DB	181	PEGDSFFIVSMCVASSVSGSKFSTOTFGCGILQDPDPANITVTAVARNRWLSVTWOD	240				
QY	241	PHSWNSSFYRLRFLRYRAERSKTFTTVMVKDLOHHCVHDAWSGLRHVVQLRAQBEFCQ	300				
DB	241	PHSWNSSFYRLRFLRYRAERSKTFTTVMVKDLOHHCVHDAWSGLRHVVQLRAQBEFCQ	300				
QY	301	GEWSEWSPGAMGTPTWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVE---	357				
DB	301	GEWSEWSPGAMGTPTWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPGRRR	360				


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; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: Neil Stahl and George D. Yancopoulos
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT APPLICATION NUMBER: US/10/287,035
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-8

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Query Match      66.2%; Score 1927.5; DB 4; Length 592;
Best Local Similarity 72.8%; Pred. No. 1.6e-143;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCALLAALAAPGAAAPRRCPAQEAVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MVAVGCALLAALAAPGAAAPRRCPAQEAVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60

QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIQLQDPPANITTVAVARNPRLWSVTWQD 240
DB 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIQLQDPPANITTVAVARNPRLWSVTWQD 240

QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWGLRHVVQLRAQEERFQ 300
DB 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWGLRHVVQLRAQEERFQ 300

QY 301 GEWSEWSPKMTPTWESRSPAEVNSTPQALTTNKDDNLLFRDSANATSLPVBFG- 359
DB 301 GEWSEWSPKMTPTWESRSPAEVNSTPQALTTNKDDNLLFRDSANATSLPVBFG- 359

QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393
DB 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393

QY 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAENNLN-----LPK 435
DB 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAENNLN-----LPK 435

QY 416 PEVKFNWVVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPA 475
DB 416 PEVKFNWVVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPA 475

QY 436 MAEKDGCQFSGFNEB-----TCLVKITGLLEFEVLEYLQON 472
DB 436 MAEKDGCQFSGFNEB-----TCLVKITGLLEFEVLEYLQON 472

QY 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529
DB 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

```

```

RESULT 5
US-10-282-162-8
; Sequence 8, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.

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; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-8

Query Match      66.2%; Score 1927.5; DB 4; Length 592;
Best Local Similarity 72.8%; Pred. No. 1.6e-143;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCALLAALAAPGAAAPRRCPAQEAVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60
DB 1 MVAVGCALLAALAAPGAAAPRRCPAQEAVARGVLTSLPGDSVTLTCGVEPEDNATVHM 60

QY 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120
DB 61 VLKPAAGSHPSRWAGMGRLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPPEPQLS 120

QY 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180
DB 121 CFRKSPLSNVVCEWGPRTSPSLTTKAVLLVRKFQNSPAEDFOEPCQYSESQKFSQCLAV 180

QY 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIQLQDPPANITTVAVARNPRLWSVTWQD 240
DB 181 PEGDSSFFIVSMCVASSVSGSKFTQTFQGGIQLQDPPANITTVAVARNPRLWSVTWQD 240

QY 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWGLRHVVQLRAQEERFQ 300
DB 241 PHSWNSFFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWGLRHVVQLRAQEERFQ 300

QY 301 GEWSEWSPKMTPTWESRSPAEVNSTPQALTTNKDDNLLFRDSANATSLPVBFG- 359
DB 301 GEWSEWSPKMTPTWESRSPAEVNSTPQALTTNKDDNLLFRDSANATSLPVBFG- 359

QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393
DB 360 -----AGLVLGQ-----FMPVPPGEDSKDVAAPHRQPL-----TSSER 393

QY 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAENNLN-----LPK 435
DB 394 IDKQIRYILDGI-----SALRKETCNKSNMCESSKEALAENNLN-----LPK 435

QY 416 PEVKFNWVVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPA 475
DB 416 PEVKFNWVVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPA 475

QY 436 MAEKDGCQFSGFNEB-----TCLVKITGLLEFEVLEYLQON 472
DB 436 MAEKDGCQFSGFNEB-----TCLVKITGLLEFEVLEYLQON 472

QY 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529
DB 476 PIEKTISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVK---GFYPSDIAVEWESN 529

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RESULT 6
US-11-134-114-8
; Sequence 8, Application US/11134114
; Publication No. US2005022033A1
; GENERAL INFORMATION:
; APPLICANT: Stahl, Neil
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: Receptor Based Antagonists and Methods of Making and Using
; FILE REFERENCE: 203C1
; CURRENT APPLICATION NUMBER: US/11/134,114
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 2001-03-22

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; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-134-114-8

Query Match 66.2%; Score 1927.5; DB 6; Length 592;
Best Local Similarity 72.8%; Pred. No. 1.6e-143;
Matches 391; Conservative 17; Mismatches 56; Indels 73; Gaps 8;

QY 1 MLAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||
DB 1 MVAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||

QY 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
|:|||||
DB 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
|:|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQEPQCYSQESQKFSQCLAV 180
|:|||||
DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQEPQCYSQESQKFSQCLAV 180
|:|||||

QY 181 PEGDSSFYIIVSMCVASSVSGSKFTQTQFCGCGILQPPPPANITTVARNRPLWSVTWQD 240
|:|||||
DB 181 PEGDSSFYIIVSMCVASSVSGSKFTQTQFCGCGILQPPPPANITTVARNRPLWSVTWQD 240
|:|||||

QY 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
|:|||||
DB 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
|:|||||

QY 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDFG- 359
|:|||||
DB 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDAG 360
|:|||||

QY 360 -----AGLVLGQ-----FMPVPPGEDSKDVNAHPHQPL-----TSSER 393
|:|||||
DB 361 EPKSCDKTHTPCCPAPALGGLGSPVFLPPKP-----KDTLMISRTPEVTCVVVDVSHED 415
|:|||||

QY 394 IDKQIRYLDGI-----SALRKETCKNSNCCSSKEALAENNLN-----LPK 435
|:|||||
DB 416 PEVKFNWVVDGVEVHNNAKTREREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 475
|:|||||

QY 436 MAEKDGFQSGFNEE-----TCLVKITGLLLEFVEYVLEYLQN 472
|:|||||
DB 476 PIEKTISKAKGQPEPVYVLTTPPSRDELTKNQVSLTCLVK---GFYPDSIAVEVESN 529
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RESULT 7
US-10-247-463-12
; Sequence 12, Application US/10247463
; Publication No. US20030082734A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timane, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE REFERENCE: DX0992Q
; CURRENT APPLICATION NUMBER: US/10/247,463
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US/09/586,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12a
; LENGTH: 468
; TYPE: PRT
; ORGANISM: primate
US-10-247-463-12

Query Match 65.8%; Score 1917; DB 4; Length 468;
Best Local Similarity 96.8%; Pred. No. 7.8e-143;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||
DB 1 MLAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||

QY 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
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DB 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
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QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQEPQCYSQESQKFSQCLAV 180
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DB 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQEPQCYSQESQKFSQCLAV 180
|:|||||

QY 181 PEGDSSFYIIVSMCVASSVSGSKFTQTQFCGCGILQPPPPANITTVARNRPLWSVTWQD 240
|:|||||
DB 181 PEGDSSFYIIVSMCVASSVSGSKFTQTQFCGCGILQPPPPANITTVARNRPLWSVTWQD 240
|:|||||

QY 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
|:|||||
DB 241 PHSNWSFYRLRFELRYRAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
|:|||||

QY 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDFGA 360
|:|||||
DB 301 GENSEWSPAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVQDSS 360
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QY 361 G-----LVLGQ 366
|:|||||
DB 361 SVPLPTFLVAGG 372
|:|||||

RESULT 8
US-10-756-149-5377
; Sequence 5377, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS A
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5377
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5377

Query Match 65.8%; Score 1917; DB 5; Length 468;
Best Local Similarity 96.8%; Pred. No. 7.8e-143;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

QY 1 MLAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||
DB 1 MLAVGCCALLAALAAAPCAALAPRCPAQAEVARGVLTSLPGDSVTLTCTGVEPEDNATVHW 60
|:|||||

QY 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
|:|||||
DB 61 VLKRPAAAGSHPSRWAGMGRLLRLRSVOLHDSGNVSCYRAGRPAGTVHLLVDVPPPEEQLS 120
|:|||||

QY 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFNQSPAEDFQEPQCYSQESQKFSQCLAV 180
|:|||||

Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Qy 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVERGA 360
Db 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDQS 360
Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372

RESULT 9

US-11-016-106-12
; Sequence 12, Application US/11016106
; Publication No. US20050106673A1
; GENERAL INFORMATION:
; APPLICANT: Dowling, Lynette M.
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and
; FILE OF INVENTION: Methods
; FILE REFERENCE: DX09920
; CURRENT APPLICATION NUMBER: US/11/016,106
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/588,113
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 12
; LENGTH: 468
; TYPE: PRT
; ORGANISM: primate
US-11-016-106-12

Query Match 65.8%; Score 191.7; DB 6; Length 468;
Best Local Similarity 96.8%; Pred. No. 7.8e-143;
Matches 360; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 1 MLVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60
Db 1 MLVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTGVHLLVDVPPPEPQLS 120
Db 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTGVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Qy 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVERGA 360
Db 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVDQS 360

Qy 361 G-----LVLG 366
Db 361 SVPLPTFLVAGG 372
RESULT 10
US-09-313-942-15
; Sequence 15, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens.
US-09-313-942-15

Query Match 65.6%; Score 191.0; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60
Db 1 MLVGCALLAALLAAPGAALAPRRCPAQEVARGVLTSLPGDSVTLTCFGEVPEDNATVHM 60
Qy 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTGVHLLVDVPPPEPQLS 120
Db 61 VLRKPAAGSHPSRWAGMGRLLRLSVQLHDSGNSCYRAGPAGTGVHLLVDVPPPEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180
Db 121 CFRKSPLSNVVCEWGPRTSLTTKAVLLVRKFQNSPAEDFQPCQYQESQKFSQCLAV 180
Qy 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIVSMCVASSVSGSKFSKTQTFQGGGILQDPDPANITVTAVARNPRWLSVTWQD 240
Qy 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Db 241 PHSWNSSFYRLRFELRYAERSKTFTTMMVKDLQHCVIHDAWSGLRHVVQLRAQEEFGQ 300
Qy 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357
Db 301 GEWSWSPFAMGTPTWTSRSPPAENEVSTPMQALTTNKDDNILFRDSANATSLPVE 357

RESULT 11

US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 360

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-15

Query Match      65.6%; Score 1910; DB 3; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Db 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Qy 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Qy 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
Db 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 12
US-10-287-035-15
; Sequence 15, Application US/10287035
; Publication No. US20030104567A1
; GENERAL INFORMATION:
; APPLICANT: NEIL STAHL AND GEORGE D. YANCOPOULOS
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203DA
; CURRENT FILING DATE: 2002-11-01
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: USSN 09/935,868
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: USSN 09/787,835
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-035-15

Query Match      65.6%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Db 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Qy 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Qy 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
Db 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 13
US-10-282-162-15
; Sequence 15, Application US/10282162
; Publication No. US20030143697A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT FILING DATE: 2002-10-28
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
; SEQ ID NO 15
; LENGTH: 360
; TYPE: PRT 4
; ORGANISM: Homo sapiens
US-10-282-162-15

Query Match      65.6%; Score 1910; DB 4; Length 360;
Best Local Similarity 99.4%; Pred. No. 1.9e-142;
Matches 355; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MVAVGCCALLAALAAPGCAALAPRCPCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Qy 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Db 61 VLRKPAAGSHPSRWAGGRLLRLRSVQLHDSGNVSCYRAGRPAGTGHLLVDVPEEPQLS 120
Qy 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Db 121 CFRKSPLSNVVCEWGPSTPSLTTKAVLLVRKFQNSPAEDFOEPCQYSQSKFSCQLAV 180
Qy 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Db 181 PEGDSSFYIIVSMCVASSVSGSKFTQTFQCGILQDPDPANITVAVARNPRWLSVTWQD 240
Qy 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Db 241 PHSNNSFYRLRFELRYRAERSKTFTTMMVKDLQHHCVIHDWNSGLRHVVQLRAQEEFGQ 300
Qy 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357
Db 301 GESEWSPAMGTPWTESRSPPAENEVSTPMQALTTNKDDNILLFRDSANATSLPVQ 357

RESULT 14
US-11-134-114-15
; Sequence 15, Application US/11134114
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10/15/01

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 7, 2006, 23:05:01 ; Search time 34 Seconds
(without alignments)
1142.592 Million cell updates/sec

Title: US-09-462-416A-13

Perfect score: 2912

Sequence: 1 MLAVGCCALLAALLAAGAAL.....LILRSKFELQSLRALRQM 553

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1871	64.3	464	6	US-10-669-920-1407
2	947.5	32.5	212	6	US-10-505-928-453
3	947.5	32.5	212	6	US-10-511-937-2489
4	947.5	32.5	212	6	US-10-933-854-11
5	927	31.8	183	7	US-11-330-917-198
6	912.5	31.3	454	6	US-10-669-920-1402
7	907	31.1	277	6	US-10-669-920-1405
8	296	10.2	368	6	US-10-449-902-38075
9	201	6.9	422	7	US-11-296-092-32
10	201	6.9	422	7	US-11-296-155-32
11	201	6.9	422	7	US-11-300-928-27
12	198.5	6.8	328	7	US-11-234-676-4
13	164.5	5.6	918	7	US-11-275-181-6
14	158.5	5.4	335	7	US-11-234-676-321
15	155	5.3	306	6	US-10-669-920-93
16	155	5.3	604	6	US-10-669-920-95
17	149	5.1	890	6	US-10-553-520-180
18	139	4.8	229	7	US-11-297-134-8
19	139	4.8	229	7	US-11-275-181-5
20	138	4.7	268	6	US-10-669-920-104
21	138	4.7	347	6	US-10-669-920-108
22	138	4.7	374	6	US-10-669-920-110
23	138	4.7	618	6	US-10-669-920-112
24	135	4.6	324	7	US-11-353-451-10
25	135	4.6	519	7	US-11-301-764-71

Sequence 6, Appli
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Sequence 5, Appli
Sequence 8, Appli
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Sequence 39, Appli
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Sequence 65, Appli
Sequence 68, Appli
Sequence 56, Appli
Sequence 325, Appli
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Sequence 305, Appli
Sequence 307, Appli
Sequence 2424, Ap
Sequence 2, Appli

US-10-669-920-1407
; Sequence 1407, Application US/106699920
; GENERAL INFORMATION:
; APPLICANT: Morritt, David W.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1407
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-1407

Query Match 64.3%; Score 1871; DB 6; Length 464;
Best Local Similarity 95.4%; Pred. No. 5.8e-135;
Matches 355; Conservative 2; Mismatches 5; Indels 10; Gaps 3;

QY 1 MLAVGCCALLAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCGVEPEDNATVHW 60
Db 1 MLAVGCCALLAALLAAGALAPRRCPAQRVAVGVLTSLPGDSVTLTCGVEPEDNATVHW 56
QY 61 VLKPKAAGSHSRWAGMGRLLLRSLVQLHDSGNYCYRAGRPAGTTHLLAVDVPPEPQLS 120
Db 57 VLKPKAAGSHSRWAGMGRLLLRSLVQLHDSGNYCYRAGRPAGTTHLLAVDVPPEPQLS 116
QY 121 CFRKSPLSNVCEWGPRTPTSLTTKAVLLVRKFQNSPAEDFQEPQCYSOESQKFCQLAV 180

ALIGNMENTS

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Db 117 CFRKSPUNVCEWGRSTSLTTNAVLVRKFNQSPAEDEQPCQSQSQSCQLAV 176
Qy 181 PEGDSSFYIVCMVASSVSGSKFTQTQFGGIIQPPPPANITVTAVARNPRLSVTWQD 240
Db 177 PEGDSSFYIVCMVASSVSGSKFTQTQFGGIIQPPPPANITVTAVARNPRLSVTWQD 236
Qy 241 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVQLRAQEBFGQ 300
Db 237 PHSWNSFYRLRFLRYRAERSKFTTMMVKDLQHCVIHDWAGSLRHVVQLRAQEBFGQ 296
Qy 301 GEWSEWPEANGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVEFGA 360
Db 297 GEWSEWPEANGTPTWTSRSPPAENEVSTPMQALTTNNKDDNIIILFRSANATSLPVDQSS 356
Qy 361 G-----LVLG 366
Db 357 SVPLPTFLVAGG 368

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RESULT 2
US-10-505-928-453
; Sequence 453, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 453
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-453

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Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVLGQGF-MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSGLGLLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRPESSEQARAVQMSKVLITQFLQKAKNLDATTTDPPTTNASLLTKLQAOQNWLQDMT 531
Db 131 NRPESSEQARAVQMSKVLITQFLQKAKNLDATTTDPPTTNASLLTKLQAOQNWLQDMT 190
Qy 532 THILRSFKFQSSLRALQRM 553
Db 191 THILRSFKFQSSLRALQRM 212

```

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RESULT 3
US-10-511-937-2489
; Sequence 2489, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald

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; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2489
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2489

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```

Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;
Matches 192; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

Qy 355 PVEFGAG--LVLGQGF-MPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKE 411
Db 11 PVAFSGLGLLVLPAAFPAPVPPGEDSKDVAAPHROPLTSSERIDKQIRYILDGISALRKE 70
Qy 412 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 471
Db 71 TCNKSNNCESSKEALAENNLNPKMAEKDGCFOGFGNEETCLVKIITGLLEFEVYLYLQ 130
Qy 472 NRPESSEQARAVQMSKVLITQFLQKAKNLDATTTDPPTTNASLLTKLQAOQNWLQDMT 531
Db 131 NRPESSEQARAVQMSKVLITQFLQKAKNLDATTTDPPTTNASLLTKLQAOQNWLQDMT 190
Qy 532 THILRSFKFQSSLRALQRM 553
Db 191 THILRSFKFQSSLRALQRM 212

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RESULT 4
US-10-933-854-11
; Sequence 11, Application US/10933854
; Publication No. US20060105347A1
; GENERAL INFORMATION:
; APPLICANT: GTC Biotherapeutics, Inc.
; APPLICANT: Meade, Harry
; APPLICANT: Cox, Geoffrey F.
; TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammals
; FILE REFERENCE: GTC-220 PCT
; CURRENT APPLICATION NUMBER: US/10/933,854
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/500,910
; PRIOR FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Human a Interferon Variant 2A
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/EMBL/DBJ Accession No. CAA00839
; DATABASE ENTRY DATE: 1993-12-03
; RELEVANT RESIDUES: (1)..(212)
US-10-933-854-11

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Query Match 32.5%; Score 947.5; DB 6; Length 212;
Best Local Similarity 95.0%; Pred. No. 6.3e-65;

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	Matches	192;	Conservative	0;	Mismatches	7;	Indels	3;	Gaps	2;
Qy	355	PVFGAG--LVGGQF-	MPVPPGSDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKE	411						
Db	11	PVAFSLGLLLVL	PAAPFAPVP	PGSDSKDVAAPHRQPLTSSRIDKQIRYILDGISALRKE	70					
Qy	412	TCNKSNNCESSKEALAENN	NLPMKAEKDCGFCQSGFNEETCLVKIIITGLLEFEFVYLYIQ	471						
Db	71	TCNKSNNCESSKEALAENN	NLPMKAEKDCGFCQSGFNEETCLVKIIITGLLEFEFVYLYIQ	130						
Qy	472	NRFESSEQARAVOMSTKVI	LQFLQKCAKNLDAITTPDPTTNASULLTKLQAQNOWLODMT	531						
Db	131	NRFESSEQARAVOMSTKVI	LQFLQKCAKNLDAITTPDPTTNASULLTKLQAQNOWLODMT	190						
Qy	532	THLILRSFKFLOSSLRQM	553							
Db	191	THLILRSFKFLOSSLRQM	212							

```

RESULT 5
US-11-330-917-198
; Sequence 198, Application US/11330917
; Publication No. US20060182716A1
; GENERAL INFORMATION:
; APPLICANT: Hong, Jin
; APPLICANT: Seiwert, Scott D.
; APPLICANT: Blatt, Lawrence M.
; TITLE OF INVENTION: Synthetic Hyperglycosylated, Protease-Resistant Polypeptide Variants
; TITLE OF INVENTION: Oral Formulations and Methods of Using the Same
; FILE REFERENCE: INTM-060W0
; CURRENT APPLICATION NUMBER: US/11/330,917
; CURRENT FILING DATE: 2006-01-11
; PRIOR APPLICATION NUMBER: 60/600,202
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/600,134
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/604,280
; PRIOR FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: 60/604,415
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 1354
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-330-917-198

```

Query Match	31.8%	Score 927;	DB 7;	Length 183;
Best Local Similarity	100.0%;	Pred. NO. 1.9e-63;		
Matches 183; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	371	VPPGEOSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNWCSSKEALAE	NN 430	
DB	1	VPPGEOSKDVAAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKSNWCSSKEALAE	NN 60	
QY	431	LNLPKMAEKGCQSGFNEETCLVKIITGLLEFVYLEYQNRPFESSEBOARAVQMSTKV	490	
DB	61	LNLPKMAEKGCQSGFNEETCLVKIITGLLEFVYLEYQNRPFESSEBOARAVQMSTKV	120	
QY	491	LIDFLOKAKNLDIAITTPDPPTTNASLLTKLQAOQNWLODMTTHILIRSFKEFLQSSLRAL	550	
DB	121	LIDFLOKAKNLDIAITTPDPPTTNASLLTKLQAOQNWLODMTTHILIRSFKEFLQSSLRAL	180	
QY	551	ROM 553		
DB	181	ROM 183		

RESULT 6
US-10-669-920-1402
; Sequence 1402, Application US/10669920
; Publication No. US20060194265A1

```

; GENERAL INFORMATION: David W.
; APPLICANT: Morris,
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1402
; LENGTH: 454
; TYPE: PR1
; ORGANISM: Mus musculus
; US-10-669-920#1402

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Query Match          31.3%; Score 912.5; DB 6; Length 454;
Best Local Similarity 49.7%; Pred. No. 8.2e-62;
Matches 187; Conservative 50; Mismatches 118; Indels 21; Gaps 9;

QY      1  MLAVGCALLAALLAAGAAALAPRRCPAQEVARGVLTSLPGDSVTLTTCGVEPEDNATVHW 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  MLTVGCTLL- -VLAAPAVVLG- -SCRALAVANGTVTSLPGATVTLICPGKEAAGNVTIHW 56

QY      61  VLKPAAGSHPSRWAGMGRILLRSVOLHDSGNYSCYRAGRAGTGHLLVADVPPPEQLS 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      57  VY-----SGSQNRWTTTGNLVLRDVQLSDTDGYLCSLNDHILVGTVPLLVADVPPPEPLS 112

QY      121  CFRKSPLSNVVCEWGPSPSTPTTKAVLLVRKFQNSPAE- DFQEPQCVSQESQKFSQCLA 179
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      113  CFRKQPLVNAICEMRPSSTPTTKAVLFAKKINTNGKSDFFQVPCQYSQQLKSFSCQVE 172

QY      180  VPEGDSFFIVSMCVASSVGSFKSTQTQGGCIIQDPDPANITVAVARNPRLWSTVWQ 239
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      173  I--GDKYHIVSLCVANSVGSKSHNEAFSLKMQQDPDPANLVLSAIGRPRPRLWKVSWQ 230

QY      240  DPHSMNSSFYRLRFELRYRAERSKTFTTWVMDLQHCVIHDWAGSLGRHWVQLRAQEEFG 299
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      231  HETWDPYYLLQFQLRYRPMVSKFTVLLLPVQYQCQVIHDALRGVHKHVQVRGKEELD 290

QY      300  QEWSEWSPSEANGTPW- TESRPPPAENEVSTPMQALTTNKKDDNILFRDSANATSL--PV 356
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      291  LGQWSEWSEVGTGTPWIAEPRTPPA--GILWNPQTVSVEDSANHDEQYESSTATSVLAPV 349

QY      357  EFGAG-----LVLGG 366
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      350  QESSMSLPTPLVAGG 365

RESULT 7
US-10-669-920-1405
; Sequence 1405, Application US/10669920
; PublicationNo. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001

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```
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-669-920-1405

Query Match      31.1%; Score 907; DB 6; Length 277;
Best Local Similarity 93.4%; Pred. No. 1.1e-61;
Matches 169; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Qy 192 MCVASSVGSKESKQTQFGCGILQDPDPANITVTAVARNPRLSVTWQDPHSNSSFYRL 251
Db 1 MCVASSVGSKESKQTQFGCGILQDPDPANITVTAVARNPRLSVTWQDPHSNSSFYRL 60

Qy 252 RFEIYRAERSKTTTVMVKDLQHCIVHDWSGLRHVVQLRAQEEFGQGEWSWSPAM 311
Db 61 RFEIYRAERSKTTTVMVKDLQHCIVHDWSGLRHVVQLRAQEEFGQGEWSWSPAM 120

Qy 312 GTPWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGAG-----LVLG 365
Db 121 GTPWTSRSPPAENEVSTPMQALTTNKDDDDNILFRDSANATSLPVEFGAG-----LVLG 180

Qy 366 G 366
Db 181 G 181

RESULT 8
US-10-449-902-38075
; Sequence 38075, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38075
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38075

Query Match      10.2%; Score 296; DB 6; Length 368;
```

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Best Local Similarity 28.0%; Pred. No. 7.1e-15;
Matches 106; Conservative 45; Mismatches 152; Indels 76; Gaps 16;

Qy 12 LLAAPGAALAPRRCPAQEVARGVLTSLPGDSVLTLCFGEVPEPDNATVHVLRKPAAGSHP 71
Db 12 VLAAGVVAYAQRH---SQQDTHVLYERLGSVDVLP-CTAAWGTAVTWVNGTDLAAHY 67

Qy 72 SRWAGMRRLLRSVQLHDSGNYSYCRAG-----RPAGTVHLLVDVPEEBOLSCFRKSPL 127
Db 68 N-----GSQLVLEGLDLSHSGHYACYGQSSWHILRYQALLH--VGMPPREPVLTCRSNSYP 120

Qy 128 SNVVCWE---GPRSTPSLTTKAVLLVRKF---QNSPAEDFQEPQCYQSQKFSQCLAVP 181
Db 121 KGFYCSWHLPSPTPIPTNTVNTVHSGSKLGCSDPA-----PKNRCHRYT 167

Qy 182 EGDSSF-YIVSMCVASSVGSKFSKTTOTFOCGILQDPDPANITVTAVARNPRLSVTWQD 240
Db 168 HLFSTVKYKVTLTVTNALGHN-STAITFDEFTIVKDPDPENNVVARPVSPRRLLEVWTQT 226

Qy 241 PHSW-NSSFYRLRFEIYRAERSKTTTVMVKDLQHC-----VIHDAWSGLRHVVQ 291
Db 227 PSSWPDPESPFLKFLRYRP-----LILDQWQHVELSDGTTHITDAYAGKEYIIQ 277

Qy 292 LRAQEEFGQGEWSWSPAMGTPW-----TESRSPPAENEVSTPMQALTTNKDDDDNI 343
Db 278 VAKDN-EIGTWSDNVAHAHATPTEPRYLTTAQAPETTTTTTSFVPPPTTKICD-- 334

Qy 344 LPRDSANATSLPVEFGAGL 362
Db 335 -----PGEVGDGV 342

RESULT 9
US-11-296-092-32
; Sequence 32, Application US/11296092
; Publication No. US20060105427A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/11/296,092
; CURRENT FILING DATE: 2005-12-07
; PRIOR APPLICATION NUMBER: US/09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
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; PRIOR FILING DATE: 2004-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-300-928-27

Query Match          6.9%; Score 201; DB 7; Length 422;
Best Local Similarity 24.7%; Pred. No. 1.5e-07;
Matches 99; Conservative 51; Mismatches 151; Indels 100; Gaps 20;

Qy 8 LLAALLAAGA-----ALAPRCPAQEVARGVLTSLPGDSVTLTCGVEPEDNATVHVW 61
Db 24 LLLCVLAPRAGSAGTAVISPODP-----TLIGSSLLATC-----SVHG- 64

Qy 62 LRKPAAGSHPSRWAGMGRLL-----LLRSVLHDSGNVSCY-RAGRP 102
Db 65 -DPGATAGLYWTLNGRLLPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSI 123

Qy 103 AGTVHLLVDVPEEP-QLSCFRKSPLSNVVCEWGP-----RSTPSTTKAVLLVRKF 153
Db 124 LAGSCLYVGLPPEKPFVNISCKN-MKDLTCRWTPGAHGETFLHTNYSLYK-----LRWY 178

Qy 154 -QNSPAEDFQPCQYSQESQKFSQCLAVPEGDSF--YIVSMCVASSVSGSKFSKTQTFFQ 210
Db 179 QGDNTCEYHTVGPH-----SCH--IPKDLALFTPEIWEATNRLGARSVDLTLDI 229

Qy 211 CGILQOPPPANITVAVARNPRWLSVTWQDPHNSWNSFYRLRPELRYRAERSKTFTTMV 270
Db 230 LDVVTTDPPDVHVRVGOLEDQSVRWVSPALKDFLQAKYQIRYRVEDS---VDMKV 286

Qy 271 KD---LQHHCVIHDAWSGLRHVVQLRAQEEFG-----QGSWSEWS-PEAMGTPWTSRS 320
Db 287 VDDVSNQTSCLAGLKPGTVFVQVRC-NPGIYGSKKAGIWSHSHPTAATPSRSPRG 345

Qy 321 P-----PAENEVSTPMQALTTNKDDDDNILPR 346
Db 346 PGGACEPRGSGPVRRELKQFLGWLKKHAYCSNLSFR 386

RESULT 12
US-11-234-676-4
; Sequence 4, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; FILE REFERENCE: 23239-578 CIP
; CURRENT FILING DATE: 2005-09-22
; PRIOR FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2004-03-05
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 4
; LENGTH: 328
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-234-676-4

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```

Query Match          6.8%; Score 198.5; DB 7; Length 328;
Best Local Similarity 24.1%; Pred. No. 1.7e-07;
Matches 81; Conservative 51; Mismatches 135; Indels 69; Gaps 14;

Qy 13 LAAPGALAPRRCPCAEVARGVLTSLPGDSVTLTCGVEPEDNATVHVLRKPAAGSHPS 72
Db 16 LASPLVAIMELKKDQVYVVDWYDPDAPGEMVLTCDTPE-EDGIT---WTU-----DQSS 66

Qy 73 RWAGMGRRLLSRVQLHDSGNYSYRAGRPAAGTVHLLV-----DV-----PPEE 116
Db 67 EVLGSCKTLTIQVKEFGDAGQYTCBKGGVLSHLLHLLKKEDGIWSTDLKQKPEKNK 126

Qy 117 PQLSRCFRKSPLSNVVCEW-----GPRSTPSLTTKAVLLVRKFKFQNSPAED 160
Db 127 TFLRCEAKNSGRFTCWMLTTTISTDLTFSVKSRRGSDPQGVTCGAATLSAERVGRDNKE 186

Qy 161 FQBPQCYQSQESQKFSQCLAVPEGDSF--YIVSMCVASSVSGSKFSKTQTFFQCGILQPPPA 220
Db 187 Y-----EYSVEQEDS---ACPAEESLPIEWMDAVHLKYENYTSFFFIIDIKPDPK 239

Qy 221 NITVTAVARNPRWLSVTWQDPHNSWNS--SPYRLRF--ELRYRAERSKTFTTMMVKDLQHH 276
Db 240 NLQLKPL-KNSRQVEVSWEYEDTWTSTPHSYFSLTFCVQVQGSKREK-----KDR--- 288

Qy 277 CVIHDWSGL-----RHVVOLRAQEEFGQGSSEWS 307
Db 289 -VFTDKTSATVICRKNASISVRAQDRYSSSWSEWA 323

RESULT 13
US-11-275-181-6
; Sequence 6, Application US/11275181
; Publication No. US20060177436A1
; GENERAL INFORMATION:
; APPLICANT: Ghilardi, Nico
; APPLICANT: Desauvage, Frederic
; TITLE OF INVENTION: METHODS FOR TREATING AUTOIMMUNE DISORDERS
; FILE REFERENCE: 11669.0240USU1
; CURRENT APPLICATION NUMBER: US/11/275,181
; CURRENT FILING DATE: 2005-12-16
; PRIOR APPLICATION NUMBER: 60/636,846
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 60/748,367
; PRIOR FILING DATE: 2005-12-06
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6
; LENGTH: 918
; TYPE: PRT
; ORGANISM: Human gp130
US-11-275-181-6

Query Match          5.6%; Score 164.5; DB 7; Length 918;
Best Local Similarity 24.8%; Pred. No. 0.00027;
Matches 57; Conservative 49; Mismatches 93; Indels 31; Gaps 11;

Qy 106 VHLLVDVPPBEPQ-LSCFRKSPLSNVVCEW-GPRST---ESLTTKAVLLVRKFKFQNSPAED 160
Db 118 ITIISGLPPEKPKNLSKIVNEG-KMRCEDWDGGRHLETNFTLKSEWATHKPAD----- 171

Qy 161 FQBPQCYQSQESQKFSQCLAVPEGDSF--YIVSMCV-----ASSVGSKFSKTQTFFQCGILQ 216
Db 172 -----CKAKRDTPT-SCTVDY-----STVYFVNIIEVWEAENALGKVTSDHINFDPVYKVKP 222

Qy 217 DPPANITVTAVARNPRWLSVTWQDPHNSWNSFYRLRPELRYRAERSKTFTTMMVKD---L 273
Db 223 NPHNLSVINSEBSLLKLTWTNPSI--KSVILKINIQRKYKDASTWSQIPPDAST 280

Qy 274 QHEHCVIHDAWSGLRHVVQLRAQEEFGQGSSEWSPEAMGTPWTE--SRSP 321
Db 281 RSSFTVQDLKPFTEYVFRICMKEDGKYSDWSEASEASGITVEDRPSKAP 330

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RESULT 14
US-11-234-676-321
; Sequence 321, Application US/11234676
; Publication No. US20060193821A1
; GENERAL INFORMATION:
; APPLICANT: Cload, Sharon T.
; APPLICANT: Diener, John L.
; APPLICANT: Ferguson, Alicia
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Keene, Sara C.
; APPLICANT: Lagasse, H.A. Daniel
; APPLICANT: Sawhney, Pooja
; APPLICANT: Thompson, Kristin
; TITLE OF INVENTION: Aptamers to the Human IL-12 Cytokine Family and Their Use as
; TITLE OF INVENTION: Autoimmune Disease Therapeutics
; FILE REFERENCE: 23239-578 CIP
; CURRENT APPLICATION NUMBER: US/11/234,676
; CURRENT FILING DATE: 2005-09-22
; PRIOR APPLICATION NUMBER: 11/075,649
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/550,962
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 60/608,046
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 323
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 321
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-234-676-321

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Query Match 5.4%; Score 158.5; DB 7; Length 335;
Best Local Similarity 21.1%; Pred. No. 0.0002;
Matches 68; Conservative 51; Mismatches 113; Indels 91; Gaps 15;

Qy 39 PGDSVTLCPGVEPDNATVHWV--LRKPAAGSHFSPRWAGMGRRLRLRSVOLHDSGNYSQ 96
Db 42 PGETVNLCTDTPEDD-----ITWTSQRHGVIGS-----GKTLTITVKEFLDAGQYTC 90

Qy 97 YRAGRPACTVHLLVDVP-----PEEPOLSCFRKSPLSNVVCEW----- 134
Db 91 HKGETLSHLLHKKENGWISTELKNFKNTFLKCEAPNYSGRFTCSMLVQRNMDLK 150

Qy 135 ----GPRSTP-----SLTTKAVLLVRKFQNSPAEDFQEPQYQSQSKFSCQ--L 178
Db 151 FNIKSSSSSPDSRAVTCGMASLSAEKVTL-----DQDYKYSVSCQBDV 195

Qy 179 AVPEGDSFPIVSMCVASSVSGSKFTOT--FOGCGILOPDPANITVTAVARNPRLSVT 237
Db 196 TCPTAETLPI--ELALEARQQNKYENYSTSFIRDIIRKPPKQLKPKNSQ--VEVS 252

Qy 238 WQDPHSNNS--SFYRLRFLRYRAERSKFTFTTMMVKDLQHCHVHDAW-----S 284
Db 253 WEYDPSMTSPHSYSLKFFVLRQKKEK-----MKETEBCNQKGAFLVEKSTEVQCK 306

Qy 285 GLRHVVQLRAQEEFGQGEWSEWS 307
Db 307 GGNVCVQ--AQDRYNNSSCSKWA 327

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RESULT 15
US-10-669-920-93
; Sequence 93, Application US/10669920
; Publication No. US20060194265A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
; FILE REFERENCE: 20366-066001
; CURRENT APPLICATION NUMBER: US/10/669,920
; CURRENT FILING DATE: 2003-09-23

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; PRIOR APPLICATION NUMBER: US 10/004,113
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 10/052,482
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/034,650
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-669-920-93

Query Match 5.3%; Score 155; DB 6; Length 306;
Best Local Similarity 22.6%; Pred. No. 0.00032;
Matches 49; Conservative 35; Mismatches 91; Indels 42; Gaps 8;

Qy 113 PPEPQLSCFRKSPLSNVVCEWGPSTSLTTKAVLLVRKFQNSPAEDFQEPQYQSQ 172
Db 20 PPGKPEIHKCRSPDKETFTTCWNNPGSGGLPTNYSL-----TYSKEGE 62

Qy 173 K--FSCQLAVPEGDSS-----FYIVSMCVASSVSGSKFTOTFQCGGILQDP 218
Db 63 KNTYECPDYKTSNGNSCFKQYTSIWKIYIITVNATNMGSTSDPLYVDVTVIVEPEP 122

Qy 219 PANIT--VTAVARNPRLSVTWQDP--HSMNSSFYRLRFLRYRAERSKFTFTTMMVKOLQ 274
Db 123 PRNLTLEVQLKDKKTYLWVKWLPPPTITDVKTGWFTMEYERLKSEEA---DEWEIHFTG 179

Qy 275ΔHHC--VIHDAWSGLRHVVQLRAQEEFGQGEWSEWSPE 309
Db 180 HQTQPKVPDLYPGQKYLVTQCKPD--HGYWSRWQGE 214

Search completed: September 7, 2006, 23:08:26
Job time : 36 secs

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